

GenCore version 5.1.6  
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Om protein - nucleic search, using frame\_plus\_p2n model  
Run on: February 15, 2005, 20:42:00 ; Search time 655.99 Seconds  
(w/o alignment) 5125.708 Million cell updates/sec

Title: US-09-904-994B-3  
perfect score: 2999

Sequence: 1 MKMKIKQEYVNTYGPTRKDKV..... KLCSTS KPTSQVPLAQRTYTFP 568

Scoring table:

BLOSUM62 Xgapop 10.0 Xgapext 0.5  
Ygapop 10.0 Ygapext 0.5  
Fgapop 6.0 Fgapext 7.0  
Delop 6.0 Delex 7.0

Searched:

4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO/spool/US0904994/rnunat 11022005.145646.25526/app\_query.fasta\_1.1102  
-DB=/cgn2\_1/USPTO/spool/US0904994/rnunat 11022005.145646.25526/app\_query.fasta\_1.1102  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFORMAT=FASTA -INFILE=ext -HEAPSIZE=5000 -MAXLEN=200000000  
-USER=US0904994@CGN\_1 -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-NO\_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7

Database :

N\_Geneseq\_16Dec04: \*  
1: geneseqn1980b: \*  
2: geneseqn1990b: \*  
3: geneseqn2000b: \*  
4: geneseqn2001ab: \*  
5: geneseqn2001ba: \*  
6: geneseqn2002ab: \*  
7: geneseqn2002ba: \*  
8: geneseqn2003ab: \*  
9: geneseqn2003ba: \*  
10: geneseqn2003cb: \*  
11: geneseqn2003dc: \*  
12: geneseqn2004ab: \*  
13: geneseqn2004ba: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2999	100.0	2883 7 ADJ58237	Adj58237 Urease subunit polypeptide complex
2	2973	99.1	2452 7 ADJ58249	Adj58249 Urease
3	2960	98.7	2405 7 ADJ58240	Adj58240 Urease
4	2953	98.5	2407 7 ADJ58246	Adj58246 Urease
5	2588	86.3	2183 7 ADJ58243	Adj58243 Urease

RESULT 1	
ID	ADJ58237 standard; DNA; 2883 BP.
XX	ADJ58237;
XX	06-MAY-2004 (first entry)
XX	Urease subunit polypeptide complex encoding sequence.
DE	immunogenic fragment; antibacterial; Vaccine; Helicobacter felis; d.
XX	KW
OS	Helicobacter felis.
XX	
KEY	Location/Qualifiers
FT CDS	205..886 /*tag= a /product= "urease polypeptide complex"
FT CDS	897..2603 /*tag= b /product= "urease polypeptide complex"
FT CDS	EP1176192-A2.
XX	
PP	30-JAN-2002.
XX	11-JUL-2001; 2001EP-00202666.
PR	17-JUL-2000; 2000BP-00202565.





Db 1879 *AGGAATAAAAGAATTGGTAGCTTCTGAGAGGGCAGATATGACACTTCGC* 1938 DR WPI; 2002-124384/17.  
 Qy 401 *IleLysArgTyrIleSerLysTyrThrIleAsnProLysLeuThrHisGlyValSerGlu* 420 DR P-PSB; ADJ58241, ADJ58242.  
 Db 1939 *ATCAACGCTTATACCTCCAAATCACCATTTCCCGTACCGTGCGACCGG* 1998 DR XX  
 Qy 421 *TrileGlySerValGluGluIleAspLeuValTrpAspProAlphe* 440 PT Disclosure: SEQ ID NO 4; 76pp; English.  
 Db 1999 *TATATCGCTCTGTGGAGAGGCGAACATGCGGACTGGTGTGGAATCTCGCTT* 2058 PT XX  
 Qy 441 *PheGlyValysProValLeuIleLysGlyGlyMetValValheSerGluMetGly* 460 PT The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis.  
 Db 2059 *T<sup>7</sup>TGGCTTAACCCAAATCTGTATCAAAGCGGTATGGTGTCTCGTAAATGGC* 2118 CC Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an ureaseXY subunit of the invention.  
 Qy 461 *AspSerAsnAlaSerValProThrProGlnProValtryTyrArgGluMetPheGlyHis* 480 CC  
 Db 2119 *GATTCATATGCCCTGCCCCCTCCAGCGGTTATTCCGGAAATTTGGCAT* 2178 CC SQ Sequence 2405 BP; 715 A; 571 C; 588 G; 531 T; 0 U; 0 Other;  
 Qy 481 *HisGlyLysAlaLysPheAspThrSerIleThrPheValSerLysValIaTyrGluAsn* 500 SQ Alignment Scores:  
 Db 2179 *CACGGCAGGCGCAATTGACCACTACGATCTGTTCCAAAGTCGCCTATGAAAT* 2238 Pred. No.: 6.82e-260 Length: 2405  
 Qy 501 *GlyVallysGluLysGluGlyLeuGluArgGlyValLeuProValysAsnCysAsnGlyAsn* 520 Score: 2960.00 Matches: 560  
 Db 2239 *GCTGTGAAGAAAAACTAGTGTAGGCTAGGCCAAAGTCGCTCCCGTGAAC* 2298 Percent Similarity: 99.30% Conservative: 4  
 Qy 521 *IleThrIlylSlysAspPheAsnAspLysThaAlaLysIleThrValAspProLys* 540 Best Local Similarity: 98.59% Mismatches: 4  
 Db 2299 *ATCACCAAGAGGACTCAAGTCACGACAAACTGCAAATCACCGTGATCGAA* 2358 DB: Query Match: 98.70% Index: 0  
 Qy 541 *ThrPheGluValPheValAspGlyLysLeuCysThrSerLysProThrSerGlnValPro* 560 DB: Gap: 0  
 Db 2359 *ACCTTCGAGGCTTGTGAGATGCAACCTCTGACCTCTAACCCACCTCTAACAGTC* 2418 Qy 21 ArgLeuGlyAspThrAspLeuTrpAlaGluValGluHisAspTyrThrThrTyrglylu 40  
 Qy 561 *IleValGlnIaTyrTyrPheHe* 568 DB: 752 CACTTGGAGATACCGATCTGGCAGAGTAGACAGTACATACACCTATAGCGAA 811  
 Db 2419 *CTAGCCCCAACGCTTACACTTTCTTC* 2442 Qy 41 GluLeuLysPheGlyValGlyLysThrIleArgGluGlyMetGlyGlnSerAsnSerPro 60  
 RESULT 3 ID ADJ58240 standard; DNA; 2405 BP. DB: 812 GAGCTCAATTGGCGCGGTAACATATCCGTGAGGTATGGTCAGAGCAATAGCCA 871  
 ID ADJ58240 standard; DNA; 2405 BP. Qy 61 AspGluAsnThrLeuAspLeuValIleAsnAlaMetIleLeuAspTyrThrGlyle 80  
 AC ADJ58240; XX DB: 872 GATGAAACACCTTACATTAGTTAGTGTGACCAACCGGAT 931  
 DT 06-MAY-2004 (first entry) Qy 81 TyrLysAlaAspIleGlyIleLysAnglyylsIleHisGlyIleGlyLysAlaGlyAsn 100  
 DE UreaseXY subunit encoding sequence #1. XX DB: 932 TATAANGCCGACATGGTATTAATGCCAAATCCATGTTATGGCAAGGGGGAAAC 991  
 KW immunogenic fragment; antibacterial; Vaccine; Helicobacter felis; ds. XX Qy 101 LysAspMetGlnAspGlyValSerProHimMetValGlyValGlyThrGluAlaLeu 120  
 OS Helicobacter felis. XX DB: 992 AAAGACATGCGATAGGCCCTCATATGGTGTGGCTGGCAAGAGCACTA 1051  
 PH Key Location/Qualifiers FT CDS 1. -681 Qy 121 AlagIgylguglyMetIleIleThrIleArgIgylgylleAspSerHisIleThrIlePhesLeuSer 140  
 FT /\*tag= a /product= "urease protein" DB: 1052 GCAGGGGAGGTATGATTAATCCGCTGCGGGATGTCGACCACTTCCTCT 1111  
 FT CDS 692. -2398 Qy 141 ProGlnGlnPheProThrAlaLeuIleAsnGlyValThrThrMetPheGlyGlyIleThr 160  
 FT /\*tag= b /product= "urease protein" DB: 1112 CCCCAACATTCCTACCGCTCTAGCCAATGGTGTACACCACATCCGGCAATGGAACTGGCACCA 1171  
 PN EP1176192-A2. XX Qy 161 GlyProValAspGlyThrAsnAlaThrIleLeuProGlyLysPhePheAlaLeuHisArg 180  
 XX PR 11-JUN-2001; 2000EP-00202666. XX DB: 1172 GGTCCGGTAGGGCACGAATGCGTACACTCCGGCAATGGAACTGGCACCA 1231  
 PR 17-JUL-2000; 2000EP-00202565. XX Qy 181 MetLeuArgIaAlaIleGluGlyTyrSerMetAsnValGlyIleLeuGlyLysGlyAsnSer 200  
 PA (ALKU ) AKZO NOBEL NV. XX DB: 1232 ATGTRGCGCGAGCTGAGATCTATGATGGCTTGGCGCAAGGCAATAGC 1291  
 PI Rusters JG. Cattoli G; XX Qy 201 SerSerIlylSlysGlnLeuValGluGlyValGluGlyValIleLeuIlePheLeuHis 220  
 DB 1292 TCCAGTAAACAAACTCGTAGAACAGTAGAGAAGCGGGCGATTCGGCTTAATGCA 1351





PT vaccines.  
 XX  
 CC Disclosure; SEQ ID NO 7; 76bp; English.  
 CC The present invention relates to a novel *Helicobacter felis* urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against *Helicobacter felis* infections and in diagnostic tests to detect antibodies against *Helicobacter felis*.  
 CC *Helicobacter felis* is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an ureaseXY subunit of the invention.  
 CC  
 XX Sequence 2183 BP; 638 A; 505 C; 550 G; 490 T; 0 U; 0 Other;  
 SQ Alignment Scores:  
 Pred. No.: 5.266-226 Length: 2183  
 Score: 2588.00 Matches: 489  
 Percent Similarity: 99.59% Conservative: 1  
 Best Local Similarity: 99.39% Mismatches: 2  
 Query Match: 86.30% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-994B-3 (1-568) x ADJ58243 (1-2183)  
 QY 1 MetlysMetlysLysGlnGluTrpValAsnThrTrpGlyProThrlysGlyAspDlyVal 20  
 Db 694 ATGAAATGAAAACAAAGTAGTGTAAACACCTGGACGCCACACAGGATAAAGC 753  
 QY 21 ArgLeuGlyAspThrAspIleUtpDlaGluValGluHiaAspTyTrThrTrpTrpGlyGlu 40  
 Db 754 CGCTTTAGGAGATCCGATCTTGCCAGAGTAGAACACTAACCTATGGCGA 813  
 QY 41 GluLeuLysPheGlyAlaGlyLysThrIleArgGlyGluMetGlyGlySerAsnSerPro 60  
 Db 814 GAGCTCAAAATTGGCGCGGCTAAACATCTCGGAGGTTGGCTCAGGCAATAGCCC 873  
 QY 61 AspGluAsnThrLeuAspIleValLeuAspAlaMetLeuIleAspTrpThrGlyIle 80  
 Db 874 GATGAAACACCTGTTAGTTAGTGTCAACACGGATGATTGACTACACGGGATT 933  
 QY 81 TyrLeuIleAspIleGlyIleLeuGlyGlyLysIleHisGlyIleGlyIleGly 100  
 Db 934 TATTAAGCCGACATGGTTAAATAATGCCAAATCCATGTTGACCCATGGCTGAGCGA 993  
 QY 101 LysAspMetGlnAspGlyValSerProHisMetValValGlyValGlyIleGly 120  
 Db 1014 TTTGGCTGAAACTAAAGATTGTCATTAAGGGCATGGTCATGGCTTCTCTGAATGGC 2073  
 QY 461 AspSerAsnAlaSerValProTrpProGlnProValtyrTrpArgGluMetPheGly 480  
 Db 2074 GATCTAACGGGCGCTGCCACCCCTCGCCGTTTACCGGAAATGTTGGGCAC 2133  
 QY 994 AACGCACTGCAAGTGGCTTAAGCCCTATATGGCTGTTGGGGACAGAGGACTA 1053  
 QY 121 AlaGlyGluGlyMetLeuIleLeuAlaGlyIleAspSerHisthRisPheLeuSer 140  
 Db 1054 GCAGGGAAAGGTATGTTATACCGCTGGGGGATCGATTCGGCAACCCACTCTCT 1113  
 QY 141 ProGlnGlnPheProThrIleLeuIleLeuGlyValThrThrMetPheGlyGlyGly 160  
 Db 1114 CCCCAACATTCCTTACCGCTCTAGCCATGGTGTACCACTCCTGGCAATGGACTCCGCC 1173  
 QY 161 GlyProValAspGlyThrAlaIleLeuGlyValGlyValGlyAlaIleGlyIle 180  
 Db 1174 GGTCGGGTAGATGCCAACGATGCCAACATCACTCCGGCAATGGACTCCGCC 1233  
 QY 181 MetLeuArgGalaIleGlyIleAspSerHisthRisPheLeuSer 200  
 Db 1234 ATGTTGCGGCAGCTGAGTAGTCTATGATGTCAGGCTTTGGCAAGGCAATG 1293  
 QY 201 SerSerIleGlyGlnIleValGluGluValGluValGlyAlaIleGlyIleLeuHis 220  
 Db 1294 TCTAGCAAAACAACTCTAGAACAGGAGCTGAGCTGTTGAGCTGGCGAATG 1353  
 QY 221 GluGlyPTPGLYIleThrProSerAlaLeuAspHisCysLeuSerValAlaPheGly 240  
 Db 1354 GAAGCTGGGCAACACAACTGAGCTGAGCTGAGCTGAGCTGGCGAATG 1413



QY 462 SerAlaSerValProThrProGlnProValTyrArgGluMetPheGlyHisHis 481  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1387 GCAATGCCTCATCCCCACTCCGAAACCGGTTAACGGGAAATGTTGGCCACAT 1446  
 QY 482 GlyLysAlaLeuPheAspThrSerIleThrPheValSerLysValAlaArgLys 501  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1447 GTTAAGGCCATTGACCAATACTTGTATCCCAAGTGCTATGACACGCC 1506  
 QY 502 ValLysGluLysLeuGlyLeuGluarginValLeuProValLysArgCysArgNile 521  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1507 ATTAAGAAGAGTrpGcgTrgCAGAAAGAGTrpGTrTrgCAGTTAAACTGCGAACATC 1566  
 QY 522 ThrlsLysAspPheLysPheAsnAspLysPheAsnAspLysPheAsnAspLysPhe 541  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1567 ACCAAAAGAACCTCAATTCAACAGTTCACGTTACCGAACATCGAATCTGAACC 1626  
 QY 542 PheGluValPheValAspGlyLysLeuCysThrSerLysProThrSerGlnValProLeu 561  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1627 TACAAGTTAAAGTGTGATGCGCAAAGAGGTACTTCCAAGCGGATAATCAGCCTA 1686  
 QY 562 AlaGlnArgTrpThrPhe 568  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1687 GCACTACTCACACTGTTC 1707

RESULT 7

ID ADQ37847 standard; DNA; 8407 BP.

XX AC ADQ37847;

XX DT 07-OCT-2004 (first entry)

DE H. bizzozeronii urease gene cluster, ureABIEFGH.

XX KW urease; urease gene cluster; ureABIEFGH; Helicobacter bizzozeronii infection;

XX KW urease; accessory gene; ureABIEFGH; Helicobacter bizzozeronii; gene; db.

OS Helicobacter bizzozeronii.

XX PN US2004142343-A1.

XX PD 22-JUL-2004.

XX PF 12-AUG-2003; 2003US-00639273.

XX PR 16-AUG-2002; 2002US-0404337P.

PA (CHAN/) CHANG Y.  
 PA (SIMP/) SIMPSON K. W.  
 PA (ZHUJ/) ZHU J.

XX PI Chang Y., Simpson KW., Zhu J.

XX DR WPI; 2004-533502/51.

DR GENBANK; AF330621.

PT Novel isolated nucleic acid molecule having urease gene cluster, and PT conferring on Helicobacter bizzozeronii ability to produce urease, useful PT as vaccine for preventing disease in mammals infected by H. bizzozeronii.

PS Claim 2; SEQ ID NO 1; 40pp; English.

XX The invention relates to an isolated nucleic acid molecule conferring on CC Helicobacter bizzozeronii an ability to produce urease, where the nucleic CC acid molecule is a urease gene cluster comprising at least one urease CC structural gene and at least one urease accessory gene. The nucleic acid molecule is chosen from ureA, ureB, ureC, ureF, ureG, ureH and ureI. The CC invention also relates to an isolated protein encoded by the nucleic acid, a vaccine for preventing onset of disease in mammals infected by H. bizzozeronii comprising a nucleic acid and a carrier, and an isolated antibody, or its binding portion raised against the nucleic acid. The nucleic acids, proteins and antibodies are useful for vaccinating mammals

CC against onset of disease caused by infection of H. bizzozeronii, which involves administering the sequence. The sequences are useful for detecting H. bizzozeronii in a sample of tissue or body fluids which involves providing a nucleotide sequence as a probe in a nucleic acid hybridization assay, contacting the sample with the antigen or the probe, and detecting any reaction which indicates that H. bizzozeronii is present in the sample. This sequence represents the H. bizzozeronii urease gene cluster, ureABIEFGH.

Sequence 8407 BP; 2264 A; 1937 C; 1969 G; 2237 T; 0 U; 0 Other;

Alignment Scores:

Pred. No. :	2,56e-201	Length:	8407
Score:	2326.00	Matches:	420
Percent Similarity:	87.30%	Conservative:	75
Best Local Similarity:	74.07%	Mismatches:	72
Query Match:	77.56%	Indels:	0
Gaps:	12		0

US-09-904-994B-3 (1-568) x ADQ37847 (1-8407)

QY    2 LysMetLysLysGlnGluProValAspThrTyrGlyProThrLysGlyAspLysValArg 21  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3068 AAAATCTCTGAAAGAATATGTTCTATGTTATGACCTACGGGCGATAATGAGA 3127  
 QY    22 LeuGlyAspThrPheLeuIlePheValGluValGluHisAspThrThrTyrGlyGluGlu 41  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3128 TTGGCGATGACGACCTATCTAGAATGCGACATGATGCTGACCAACTATGCCGAGAA 3187  
 QY    42 LeuGlyAspGlyAlaGlyLysThrIleArgGluGlyMetGlyInserAnsProAsp 61  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3188 ATTAAAGTTGTGCGGGAAACATTGCGATGGATGGACAGAACACAGCCCCAGC 3247  
 QY    62 GluLysThrIleAspLysPheValIleThreonAlaMetIleLeuAspTyThrGlyLeuTyr 81  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3248 AGCCACGAACTCGAATCTCTGCTACTACGACATGCTGATCTGGATTACCGGACATTAT 3307  
 QY    82 LysAlaAspIleGlyIleLysAsnGlyIleIleHisGlyIleGlyLysAlaAsnGly 101  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3308 AAACCGGATATTGGCATTAATGGCAAATCCATGGCATGGCAAGCAGGCAATAAA 3367  
 QY    102 AspMetGlnAspGlyValSerProHisMetValValGlyValGlyThrGluAlaLeuAla 121  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3368 GACATGCAAGATGGCGTTCACATCTTGTGCGTGGCCCTCTACAGGTTGGCC 3427  
 QY    122 GlyLysLysMetIleIleThrIleArgLysGlyIleAspSerHisThrIlePheLysSerPro 141  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3428 GCTGAAGGCGCTGATGTCAGCTGGTGGAGCACCCACATCCACTTATTCCTCC 3487  
 QY    142 GluGlnPheProThrAlaLeuAlaAsnGlyValThrIleMetTheGlyGlyGlyThrGly 161  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3488 CAACAAATCCCACAGCATTTGGCGCGGATCACACATGATGTTGGGGGACAGCT 3547  
 QY    162 ProValAspGlyThrAspAlaIleThrIleThrProGlyLysTrpAspLeuHisArgMet 181  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3548 CCAGCTGTAGGGACTAACGGATACCTACTCCAGCTGGAGCATTTAAATCCACCA 3607  
 QY    182 LeuArgGlnAlaGlyLysIleSerMetIleValGlyIlePheLeuIleGlyIle 201  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3608 CTCTGGCTCTGAGAATGCTGTTAAACCTTGCT 3667  
 QY    202 SerLysLysGlnLeuValGluAlaGlyAlaLeuGlyPheLysLeuHisIle 221  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3668 TATGAACTCCCTGGTGTGATCAACTCCAGCTGGAGCATTTAAATCCACCA 3727  
 QY    222 AspPheGlyThrIlePheSerAlaLeuPheAspGlyLysAsp 241  
   : : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 3728 GACTGGGGTAGACCTGAGCATCTTACCTGCTGTTGAATGCGGAGAACATGGAT 3787  
 QY    242 ValGlnValCysLeuIleThrAspThrValAsnGlyIleGlyIleValAspAspThrIle 261  
 CC 3788 GTGCAAGTGGCTATCCACACCGATACCTGATGAAAGGGCTGTTGAGAACACTTG 3847

DT 21-SEP-1990 (first entry)  
 XX DE Probe for sequence encoding part of protein with urease activity.  
 XX KW Urease; probe; ss.  
 XX OS Helicobacter pylori.  
 XX PN WO904030-A.  
 XX PD 19-APR-1990.  
 PF 06-OCT-1988; 88FR-00013135.  
 XX PR 06-OCT-1988; 88FR-00013135.  
 XX PA (INSP ) INST PASTEUR.  
 PA (INRM ) INSERM INST SANTE & RECH MED.  
 XX PI Labigne A;  
 XX DR MPI; 1990-147844/19.  
 DR P-PSDB; AAK04580.  
 PT New nucleotide sequences encoding *Campylobacter pylori*-ureaseents - and  
 derived vectors, transformants, protein, antibodies and probes, useful in  
 diagnosis, treatment and prevention of infections.  
 XX PS Claim 7; Page 32; 47pp; French.  
 CC Detection probes consisting of all/part of the sequence can be used to  
 detect *C. pylori* in stomach biopsy samples. The DNA can also be used  
 to express proteins for the prodn. of antibodies and to prepare vaccines.  
 CC See also AAQ04309, AAQ04311, AAQ04328-30 and AAQ04581. (Updated on 25-MAR  
 -2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS  
 field)  
 CC XX Sequence 1710 BP; 537 A; 365 C; 387 G; 421 T; 0 U; 0 Other;  
 SQ Alignment Scores:  
 Pred. No.: 1.36e-199 Length: 1710  
 Score: 2297.00 Matches: 416  
 Percent Similarity: 86.77% Conservative: 76  
 Best Local Similarity: 73.37% Mismatches: 75  
 Query Match: 76.59% Indels: 0  
 DB: Gaps: 0  
 US-09-904-994B-3 (1-568) x AAQ04329 (1-1710)  
 Qy 2 LysMetLysysGlnIleThrValAsnThrTyrGlyProThrLysGlyAspLysValArg 21  
 Qy 7 NAGATTTAGCAGAAAAGAAATATGTGTTCTACTATGGCTTAAGTGAGA 66  
 Db 522 ThrlsLysysAspPheLysAspLysIleAspLysIleThrValAspProLysThr 541  
 Db 4628 ACCAAANAAAGACCTCAATTCAACGATGTACCGCACACATCGAAGTCATCTGAACC 4687  
 Qy 42 LeuLysPheGlyAlaLysLysThrLeuCysThrSerLysProThrSerGlnValProLeu 561  
 Db 4688 TCAAAAGCTTAAGTAGGAGGAGGTACTTCGAAGCGGGATAAAATCAACCTCA 4747  
 Qy 562 AlaGlnArgThrThrPhePhe 568  
 Db 4748 GCAAACTCTAACATTGTTTC 4768  
 RESULT 8  
 AAQ04329 ID AAQ04329 standard; DNA; 1710 BP.  
 XX AC AAQ04329;  
 XX DT 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)









Db 2508 GCGCACTCTTGGATTTTC 2528

RESULT 12

AAL60579  
ID AAL60579 standard; DNA; 1710 BP.  
XX  
XX  
AC AAL60579;  
XX  
DT 03-SEP-2003 (first entry)  
XX  
DE Helicobacter pylori urease B (ureB) DNA.  
KW Recombinant protein; plant pollen; urease B; ureB; ds.  
XX  
OS Helicobacter pylori.  
XX  
RN WO2003044050-A1.  
XX  
PD 30-MAY-2003.  
XX  
PF 19-NOV-2002; 2002WO-KR002154.  
XX  
PR 19-NOV-2001; 2001KR-00071712.  
XX  
PA (PARK/) PARK H.  
XX  
PT Park H;  
XX  
DR WPI; 2003-457520/43.  
XX  
PT Producing a recombinant protein using plant pollen, for industrial uses,  
PT comprises introducing a target gene into an Agrobacterium vector, and  
infecting the transformed Agrobacterium into a cultured plant pollen.  
XX  
PS Example 1; Page 29-30; 34pp; English.

CC The invention relates to a method of producing a recombinant protein  
CC using plant pollen. The method involves introducing a target gene into an  
CC Agrobacterium vector and infecting the transformed Agrobacterium into a  
cultured plant pollen. The method is useful for producing recombinant  
proteins for testing, diagnosis and prevention and for industrial use.  
CC The present sequence is Helicobacter pylori urease B (ureB) DNA. This  
CC sequence is used in the exemplification of the invention  
XX

SQ Sequence 1710 BP; 540 A; 371 C; 383 G; 416 T; 0 U; 0 Other;

Alignment Score:  
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Score: 2291.00 Matches: 415  
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 CC :|||:|||||:|||||:|||||:|||||:|||||:|||||:  
 CC 482 GlyTyIleAlaSpheAspThrSerIleThrPheValSerIleValAlaGluArgGly 501  
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 Job time : 703.99 secs



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DEFINITION Sequence 1 from Patent EP1176192.

ACCESSION AX356683  
VERSION AX356683.1 GI:18674020

KEYWORDS Helicobacter felis

SOURCE Helicobacter felis

ORGANISM Helicobacter; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.

REFERENCE 1 Kusters, J.G. and Cattoli, G.

AUTHORS Helicobacter felis vaccine

TITLE Patent: EP 1176192-A 130-JAN-2002;

JOURNAL Akzo Nobel N.V. (NL)

FEATURES location/Qualifiers

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ORIGIN

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score: 100.00%

percent Similarity: 100.00%

Best Local Similarity: 100.00%

Match: 6

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US-09-904-994B-3 (1-568) x AX356683 (1-2883)

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Qy 301 ProThrIleProThrIleLeanThrValAlaGluHisAspLeuAspMetLeuMetThrGly 320  
Db 1797 CCCATTCATCCCTACCATTAATGCTTGCGAGCTTGACCTTGACATGCC 1856

Qy 321 HisIleIleAspIysSglIysTgIleArgGluIysPheGlnPheSerGlnSerArgIleArg 340  
Db 1857 CACCACTTACGACAACGATCCCGCAGATTACAATTTCGAAGCGTATCCGCC 1916

Qy 341 GlySerIleAlaAlaGluAspValLeuHisAspMetGlyValLeuAlaMetThrSer 360  
Db 1917 GGCTCTATGGGCGCTGAAGATGTCCTCATGATATGGCTGTGATGCCAGAACGCG 1976

Qy 361 AspSerGlnAlaMetGlyArgAlaGlyIleValIleProArgIleGlyGlnThrAlaP 380  
Db 1977 GATTCGAGCATGGCGCTGCGCATGCGCAT 2036

Qy 381 LysAsnIlysLysGluPheGlyIlysLeuProGluAspGlyIysAspAspAspPheIg 400  
Db 2037 AAGATAAAAGATTTGGTAGCTCTGAGATGGCAGATAAGATAATTCCGC 2096

Qy 401 IleLeuIysPheGlyIleLeuAspLeuValIleThrAsnAlaMetIleLeuAspThrThrGlyIle 420  
Db 2097 ATTAGCCTACACTCCAAATCAACCCGCTTGGACCGACGGCTGAGCG 2156

Qy 421 TyrIleGlySerIleGluGlyIleLeuAspLeuValIleThrAsnAlaMetIleLeuAspThrThrGlyIle 440  
Db 2157 TATATGCGCTCTGGAGGAGGCAAGATCGCGCACTGGCTGCTT 2216

		Alignment Scores:	
	Pred. No.:	Length:	2452
QY	441 PhiegelvallylprolysileValleyleValleyleGlylMetValValPheSerGluMetGly	460	2452
Db	2217 TTGGCTTAACCCAAATCTGCAAGGGATGGCTCTCTGAATGGC	2276	562
QY	461 AspSerAsnAlaSerValProThrProGlnProValProValTyrArgGluMetBpheGlyHis	480	4
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QY	481 HisGlyLysAlaLysPheAspThrSerLeuThrPheValSerLysValAlaTyrGluAsn	500	0
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QY	501 GlyVallylsglyllysteaughlylueaughlylarginValleuProVallylsasnCysBargAsn	520	99.65%
Db	2397 GCGCTGAAGAAAGCAGCAGCTAGAGCAGCTAACGTCAAAATGCGCTAAC	2456	98.94%
QY	521 IleThrIyslvsAspPhelylspheAsnAspLyslserThralalyslserLeuValAspLys	540	99.13%
Db	2457 ATCACCGAAGAAGCTCAAGTCACAAGCACAGCAAAATCACCGTCATCCGAA	2516	6
QY	541 ThrPheGluValPheValAspLyslsglyllyleuCysThrserValProValPro	560	Gap:
Db	2517 ACTTCGAGGTCTTGTAGATGCAAACTCTCACCTCAACCTCGAAAGTGCCT	2576	
QY	561 LeuAlaGlnNAGTyrThrPhePhe	568	
Db	2577 CTAGCCCAGCCTACATTCTTC	2600	
RESULT 3			
LOCUS	BD185306	2452 bp	DNA
DEFINITION	Helicobacter felis vaccine.	1	linear
ACCESSION	BD185306		PAT 17-JUN-2003
REFERENCE	1 (bases 1 to 2452)		
VERSION	BD185306_1		
AUTHORS	Kusters,J.G. and Cattoli,G.		
TITLE	Helicobacter felis vaccine		
JOURNAL	Patent: JP 2002355054-A/5.		
ORGANISM	Helicobacter felis		
BACTERIA	Proteobacteria; Epsilonproteobacteria; Campylobacterales;		
REFERENCE	21 ArgLeuGlyLysPheAspLeuTrpAlaLysValGluHisAspTyThrThrTyrGlyGlu		
VERSION	BD185306		
KEYWORDS	BD185306_1		
SOURCE			
COMMENT			
OS	AKZO NOBEL NV		
PI	Helicobacteridae; Helicobacter.		
PD	10-DEC-2002		
PP	16-JUL-2001		
PR	17-JUL-2000		
PC	JOHANNES GERARDUS KUSTERS, GIOVANNI CATTOLI		
C12N15/09, A61K38/00, A61K39/106, A61K39/118, A61K39/12, A61K39/175, PC			
PC	A61K39/23, A61K39/235, A61K39/3, A61K39/395, A61P1/04, A61P31/04, C12N1/15, C12N1/19,		
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PC	G01N33/53, G01N33/66, G01N33/569 / (C12N9/80, C12R1.01), (C12O1/68, PC		
PC	C12R1.01), C12N5/00, C12N5/00, A61K37/02		
CC	Helicobacter felis vaccine		
FH	Location/Qualifiers		
KEY	(49). .(728)		
FT	CDS (739). .(2445).		
FEATURE	location/Qualifiers		
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Qy 341 GluSerIleAlaAlaGluSpValLeuHsAspMetGlyValLeuAlaMetThrSer 360  
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 Qy 361 AspSerGlnAlaMetGlyArgAlaGlyGluValLeuProArgThrTrpGlnThrAlaAsp 380  
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CDS

Qy 381 LysAsnLysLysGluPheGlyIleLeuProGluAspGlyLysAspAspAspPheAsp 400  
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 Db 1939 ATCAAACGCTTATCTCCAATACACCAATTATCCCGCTTGACCCATGGCGAGCGAG 1998

Qy 421 TyrIleGlySerValGluGlyGlyLysIleAlaAspLeuValIleTrpAsnProAlaPhe 440  
 Db 1999 TATATCGGCTCTCGAGAGCAGGCGAAAGTGGCCACTTGCTGGCTGGTGGATCCGCC 2058

Qy 441 PheGlyValysProLysIleValIleLysGlyGlyMetValValPheSerGluMetGly 460  
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Qy 461 AspSerAlaSerValProThr-ProGlnProValProIleThrArgGluMetPheGlyHis 480  
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Qy 481 HisGlyLysValIysPheAspThrSerIleThrPheValSerIysValAlaArgLys 500  
 Db 2179 CACGGCAAGGCAGATTGCAACGACGACATTTGCTCAAGTCGAACT 2238

Qy 501 GlyValysGluIysLysLeuGlyLeuGluArgIleValProValPheAspCysBargan 520  
 Db 2239 GGTGTGAAAGAAACTAGTTGAGGCCAGGTGCTCCCGTGAAGAACTGGCTAAC 2298

Qy 521 IleThrIlyValysAspPheAspAsnIlysThrIleAlaIleAspIleThrValAspIle 540  
 Db 2299 ATCACACCAGAAGGACTCTCAAGTCAACGACAACATGCAAAATCACCTCGATCGAA 2358

Qy 541 ThrPheGluValIlePheValAspGlyLysIleAspCysThrSerIysProThrSerGlnValPro 560  
 Db 2339 ACCCTCGAGGTCTTGTGATGCAACTCTGCACCTCTAAACCCACCTCTGAAGTGCCT 2418

Qy 561 LeuAlaGlnArgTyrThrPhePhe 568  
 Db 2419 CTAGCCCCAAACGCTAACACTTCTTC 2442

RESULT 4

AX356695 LOCUS AX356695 DEFINITION Sequence 13 from Patent EP1176192. ACCESSION AX356695 VERSION 1.1.18674032 KEYWORDS SOURCE Helicobacter felis ORGANISM Helicobacter felis

REFERENCE AUTHORS Kusters,J.G. and Cattoli,G. TITLE Helicobacter felis vaccine Patent: EP 1176192-A 13-JAN-2002; JOURNAL Akzo Nobel N.V. (NL) FEATURES location/Qualifiers 1. 1.2452 /organism="Helicobacter felis"

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ORIGIN

Alignment Scores:

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Best Local Similarity:	98.94%	Mismatches:	2
Query Match:	99.13%	Index:	0
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US-09-904-994B-3 (1-568) x AX356695 (1-2452)

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 Db 739 ATGAAATTGAAAAACAAAGAGTAGTGAATAACTACGACCCACAGCGGATAAATG 798

Qy 21 ArgIleGlyYaspThrAspLeuTrpAlaGluValGluHisAspPheTyrrThrThrGlyIle 40  
 Db 799 CGCTTAGGAGATCCGCTTGGCAGAGTGACTGACTGACATACCCATGGCGA 858

Qy 41 GluIleIysPheGlyIaGlyIysThrIleArgGluGlyMetGlyGlnSerAsnSerPro 60  
 Db 859 GAACTCATTCGCTGCGGTAAACTATCCGGAGGTATGGTCAAGCAATAGCCCA 918

Qy 61 AspGluIaanthrIleAspLeuValIleThrAsnAlaMetIleLeuDPTyrrGlyIle 80  
 Db 919 GATGAAACACCTAGATTAGTGTACCAACGGGATGATATGACTACCGGGTT 978

Qy 81 TYIVLYSAlaAspIlePheGlyIleLeuBASGlyYaspIleLeuHsGlyIleGlyGlyYaspIle 100  
 Db 979 TACAAAGGAGACATGCGATTAACGCAAAATCCCTGGCATGGCAAGCGGAAAC 1038

Qy 101 LYIaspMpeGlnAspGlyValSerProIleMetValValGlyValGlyYaspIle 120  
 Db 1039 AAGGACATCCAGAGGGCTAAGCCCTTAATGTCGTTGGGTGGGGACAGAGCA 1098

Qy 121 AlgiLyGlyGlyIleIleIleThrIleIleGlyIleAspSerSerIleIleIleIle 140  
 Db 1099 GCAGGGAGGATGATATTACCGCTGGGGACACCCACTCTCTCT 1158

Qy 141 ProGlnGlnPheThrThaLeuIaLysGlyValThrMetPheGlyIleGlyThr 160  
 Db 1159 CCACACATTCCTACCGCTTACGCAATGGCTGCGGTGCA 1218

QY	161 GlyProValAspGlyThrAspAlaThrIleThrLeuProGlyLysTrpAsnLeuIleSarg 180	Db	2299 ATCACCAAGAGGACTCAGTTCAGCACAATACCGCTGATCGAA 2358
Db	1219 GCCCCGGTAGTGCGACAGTCGACTTACCTGCGCCAACTGACCGC 1278	QY	541 ThrPheGluValPheValAspGlyLysLeuCysteSerylProThreonineValPro 560
QY	181 MetLeuArgIlaAlaLagIluGluLysSerMetAsnValGlyPheLeuIlyLysLeuSer 200	Db	2359 ACCTCGGAGCTTGATGGCAACTCTGCACCTCTAACCCACCTTGAAAGTGCT 2418
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QY	201 SerSerIlysLysGlyLeuIleValGluGlyValAlaGlyAlaLeuIlePheIleHis 220	Db	2419 CTAGCCAAACCTACACTTCTTC 2442
Db	1339 TCTAGTAAACAACTGTGAGAACAGTAGAGCAGGCGCATGGTTTAATWGT 1398		
QY	221 GluAspTrpGlyThrThrProSerAlaLeuAspPhiCysLeuSerValAlaAspGluThr 240		RESULT 5
Db	1399 GAAGACTGGGCCACAATCCGAACTCCAGTGGCATCCTACTGCTGCTAGCTGAGATAAC 1458	BD185303	BD185303
QY	241 AspValGlnValCysIleHisIleThrAspThrValAsnGluAlaGlyTyValAspThr 260	LOCUS	DEFINITION Helicobacter felis vaccine.
Db	1519 CTAATGCAATGAACTGGCCGCCCCATCATGCTACCTACACATGAGGGATGAGATGAC 1518	ACCESSION BD185303	ACCESSION BD185303.1 GI:31877503
QY	281 HisSerProAspValIleIleMetAlaGlyGluLeuAsnIleLeuProSerSerThrThr 300	VERSION BD185303.1	VERSION JP 2002355054-A/2.
Db	1579 CACTCACCTGATGTTATCACCTGGCGAGGAGATTCACCTCCCTCCACAAACC 1638	SOURCE	SOURCE Helicobacter felis
QY	301 ProThrIleProTyThrIleAsnThrValAlaGluHisLeuAspMetLeuMetThrCys 320	ORGANISM	ORGANISM Helicobacter felis
Db	1639 CCTACTATCCCTATCATTATAAGTGTGGAGAACACTTGACATGCTTATGACTGC 1698	REFERENCE	REFERENCE Helicobacter felis vaccine
QY	341 GlySerIleAlaAlaGluAspValLeuHisAspMecGlyValIleAlaMetThrSer 360	AUTHORS	AUTHORS Helicobacter felis vaccine
Db	1759 GCTCTCTATCGCGCTGTGAGATGTGTCATGATCGCTGAGATCGCGATGACAGTTC 1818	TITLE	TITLE Helicobacter; Proteobacteria; Bspilonproteobacteria; Campylobacterales; Bacteri; Proteobacter; Helicobacter
QY	361 AspSerGlnAlaMetGlyArgIlaGluAspIleGlnIpheSerGlnSerArgIleArgPro 340	JOURNAL	JOURNAL 1 (bases 1 to 2405)
Db	1699 CACCACTCTAGATAAACCGATCCGGAGAGATCTCCAAATTCTCAAGCCGTAACTCCCCC 1758	COMMENT	COMMENT 1 (bases 1 to 2405)
QY	341 GlySerIleAlaAlaGluAspValLeuHisAspMecGlyValIleAlaMetThrSer 360	PATENT	PATENT 1 (bases 1 to 2405)
Db	1759 GCTCTCTATCGCGCTGTGAGATGTGTCATGATCGCTGAGATCGCGATGACAGTTC 1818	PERSON	PERSON 1 (bases 1 to 2405)
QY	381 LysAsnIlysLysGluIlePheGlyIlysLeuProGluAspGlyIlysAspAsnAspIleArg 400	OS	OS 1 (bases 1 to 2405)
Db	1879 ALGAATTAAGAAGATTGGTGTAGCTCTGAGATGTGCGATATGACACTCCGC 1938	PN	PN 1 (bases 1 to 2405)
QY	401 IleIlyArgTyIleSerIlysTyThrIleAsnProIleIleThrIlyGlyValSerGlu 420	PD	PD 1 (bases 1 to 2405)
Db	1939 ATCAAAGCTATATCTCCAATACACATTAAACCCATTGACCGTGAACGG 1998	PF	PF 1 (bases 1 to 2405)
QY	421 TrileGlySerValGluGluGlyIlysIleLeuAspIleValValTPasnProAlaPhe 440	PT	PT 1 (bases 1 to 2405)
Db	1999 TATATCGGCTCTGTGGAGAGAGCGACATGGCTGGTGTGAACTCTCGCTT 2058	PC	PC 1 (bases 1 to 2405)
QY	441 PheGlyValIleProIleValIleIlyGlyGlyMetValValPheSerGluMetGly 460	PC	PC 1 (bases 1 to 2405)
Db	2059 TTGGCCCTAAACCCAAATCTGTGATCAAGCCGATGGTGTCTCTCAAATGGC 2118	CC	CC 1 (bases 1 to 2405)
QY	461 AspSerAsnAlaSerValProThrProGlnProValProTyArgGluMetPheGlyHis 480	Key	Key 1 (bases 1 to 2405)
Db	2119 GATCTCTATGGCTCTGCCCCACTCTCAGCGGTATTACCGCGAAATGTTGGCAT 2178	FT	FT 1 (bases 1 to 2405)
QY	481 HisGlyIlysAlaLysPheAspThrSerIleThrPheValSlyValAlaTyGluasn 500	CDS	CDS 1 (bases 1 to 2405)
Db	2179 CAGGGCHAGGCCAAATTGACCAAGCATCACCTTGTCCTGAAATGAAAT 2238	FEATURES	FEATURES 1 (bases 1 to 2405)
QY	501 GlyValIlysGluIlysIleGlyIleGluIleGluGlnValLeuProValAsnCysArgAsn 520	source	source 1 (bases 1 to 2405)
Db	2239 GGTTGTAAGAAGAAACATGGTTAGGCCAGGTCTCCCGTGAAGATGCCAAC 2298	ORIGIN	ORIGIN 1 (bases 1 to 2405)
QY	521 IleThrIlysLysAspPheAsnAspIlysPheAsnAspIlysPheAsnProLys 540		
Db	752 CGCTTAGGAGATACCGATCTTGGSCAGAGTAGAGTAGACTAATACCACTATCGCAA 811		



ORIGIN

Alignment Scores:		Length:		Score:	
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		Conservative:	560		
Best Local Similarity:		Mismatches:	4		
Query Match:		Indels:	0		
DB:		Gaps:	0		
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Qy	21 ArgLeuGlyAspThrAspLeuUTPAlaGluValGluHisAspThrThrThrTyroGlu				
Db	752 CCGTTAGGAGATCCGACTTGGCAGAGTGAGCACTACATACCTATTGCGA				
Qy	41 GlutLeuLysPheGlyAlaGlyLysThrIleArgGlyLysMetGlyGlnSerPro				
Db	812 GAGCTCAATTGCGCCGGCTAACTATCCGTGGGATGCGTACAGCAATGCCA				
Qy	61 ArgGluAsnThrLeuAspLeuValIleThrAspAlaMetLeuIleAspThrGlyIle				
Db	872 GATGAAAAACACTTGAATTAGTTAGTGATCACCAACGGATGATTAGCTACACGGATT				
Qy	81 TyroSalaAspIleGlyIleLeuBamGlyLysIleHsGlyIleGlyIleGlyYbaGlyAsn				
Db	932 TATAAASCAGCATTTGTATTAAATGCGCAAATCCATGTTATGGCAGGGAACT				
Qy	101 LysAspMetGlnAspGlyValSerProHisMetValValGlyValGlyThrGluAlaLeu				
Db	992 AAGGACATGCCAGATGGCCTAACGCCCTATGGCCTGGGTGGGCAGAGCAGCACTA				
Qy	121 AlaGlyGluGlyMetIleIleThrAlaGlyGlyIleLeuSerSerHisThrIlePhoLeuSer				
Db	1052 GCAGGGGAGGATGATTATACCGCTGGGGAGATGGCAGACCCACTTCCTCT				
Qy	141 ProGlnGlnPheProThrAlaLeuAlaGlyValThrThrMetPheGlyGlyLysThr				
Db	1112 CCCACAATTCCTACGGCTTAGCCAATGGCTTACACCAGTTGGAGGGCACA				
Qy	161 GlyProValAspGlyThrAlaIleThrThrIleThrProGlyLysTrpAlaLeuHisArg				
Db	1172 GGTCGGGATGATGCCACGAGTCGCCACCATCTCCGGCAATGGCACTGCCCG				
Qy	181 MetLeuArgAlaIleGluIleTyrSerMetAsnValGlyIleLeuGlyAlaIleGlyIleLeuHis				
Db	1232 ATGTTGGCGCAGCTTATGATGATGIGGGCTTGGCAGAGGATAG				
Qy	201 SerSerIleLysGlnLeuValGluGlyValGlyAlaGlyAlaIleGlyIleLeuHis				
Db	1292 TCCAGTAACAAACTCTAGAACAGAACTGAGAGCTTAAATGCT				
Qy	221 GluAspPheGlyThrThrProSerAlaLeuAspHisCysLeuSerValAlaAspGluThr				
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Db	1472	CTAAATGGATGACGGCGGCCCATCCTACGCTACACATGAGGAGCGGCAGGA	1531
Qy	281	HisSerProAspValleAlaLleThrmetaIaglygluLeuasnIleLeu	300
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Qy	301	ProThrLeProTyrrThrIleAsnTrvallagluHisLeuAspMetLeu	320
Db	1592	ThrCysCCCACTATCCCTATACCATTAATACGTTGCGAACACTTAGACTG	1651
Qy	321	HisBisIeuIaspIleAspargIleArgIluAspIeuglnPheSerGlnSer	340
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Qy	341	gIySerIleAlaAlaGluAspValleUhiAspMetGlyValleAlaMet	360
Db	1712	ThrSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer	1771
Qy	361	AspSerGlnAlaMetGlyArgAlaGlyGluValleProAspGlyLea	380
Db	1772	GATTCGCKAGCATGGCGCCGCTGGCGAAGTGGATTCTGAGCTGAGAC	1831
Qy	381	LysAsnIyslsgluIpheGlyIysluIpheGlyIysluIpheGlyIys	400
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Qy	401	IleLySArgTyrlleSerLySArgTyrlleSerLySArgTyrlleSer	420
Db	1892	ThrIleAsnProAlaLeuThrIleAsnProAlaLeuThrIleAsnPro	1951
Qy	421	TyrIleGlySerValIgluIgluIgluIgluIgluIgluIgluIgluI	440
Db	1952	TATATGCTCTCTGCTGAGGAGGCAATCGCGCAATCGCGCAATCGCG	2071
Qy	441	PheGlyIvallysProlysProlysIleAspIleAspIleAspIleAsp	460
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Db	2132	IleAspSerAlaSerValProThrProGlnProValIleIleAspSerAla	2191
Qy	501	GlyIvallysGlyIysIleGlyIysIleGlyIysIleGlyIysIleGly	520
Db	2192	GCGTGAAGAAACATAGGCTTAGAGCGCAGGCTCTACCGTGAAACTGCC	2251
Qy	521	IleThryIysIleAspPhelysPheAsnAspIysThaAlaIysIleThrValAsp	540
Db	2252	PheAspIysIleAspPhelysPheAsnAspIysThaAlaIysIleThrValAsp	2311
Qy	541	Tir-PheGluValPheValAspGlyIysIleCysIysSerIysProThrSer	560
Db	2312	IleGluValPheValAspGlyIysIleCysIysSerIysProThrSerIys	2371
Qy	561	IleAlaGinIargTyrrThrPhePhe	568
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LOCUS	He1cobacter felis vaccine.		
DEFINITION			
ACCESSION	BD185305		
VERSION	BD185305.1	GI:318777505	

KEYWORDS JP 2002355054-A/4.  
 SOURCE Helicobacter felis  
 ORGANISM Helicobacter felis  
 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 REFERENCE 1 (bases 1 to 2407)  
 AUTHORS Kusters, J.G. and Cattoli, G.  
 TITLE Helicobacter felis vaccine  
 JOURNAL Patent: JP 2002355054-A 10-DBS-2002;  
 AKZO NOBEL NV  
 COMMENT OS Helicobacter felis  
 PN JP 2002355054-A/4  
 PD 10-DEC-2002  
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 PI JOHANNES GERARDUS KUSTERS, GIOVANNI CATOLI  
 PC C12N15/09, A61K39/00, A61K39/106, A61K39/118, A61K39/12, A61K39/175, PC  
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 LOCUS AF330621 Helicobacter bizzozeronii tRNA ribosyltransferase gene, partial  
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 ACCESSION AF330621  
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 KEYWORDS  
 SOURCE Helicobacter bizzozeronii  
 ORGANISM Helicobacter bizzozeronii  
 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 Helicobacteraceae; Helicobacter.  
 REFERENCE 1 (bases 1 to 8406)  
 AUTHORS Zhu,J., Tang,C.H., Chang,C.F., Simpson,K.W., Wei,C., McDonough,P., McDonough,S. and Chang,Y.R.  
 TITLE Cloning and characterization of a Helicobacter bizzozeronii urease gene cluster  
 JOURNAL DNA Seq. 13 (6), 321-331 (2002)  
 MEDLINE 12652903  
 PUBMED 2 (bases 1 to 8406)  
 AUTHORS Zhu,J. and Chang,Y.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-DEC-2000) Population Medicine and Diagnostic Science,  
 College of Veterinary Medicine, Cornell University, Tower Road,  
 Ithaca, NY 14853, USA  
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ORIGIN				
Allignment Scores:				

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ACCESSION AY295085		
VERSION AY295085.1 GI:31580720		
KEYWORDS		
SOURCE		
ORGANISM	Helicobacter pylori	
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;		
Helicobacteraceae; Helicobacter.		
REFERENCE 1 (bases 1 to 1710)		
AUTHORS Duan, G.C. and Dai,L.P.		
TITLE Direct Submission		
JOURNAL Submitted (11-MAY-2003) Epidemiology, College of Public Health,		
REFERENCE 2 (bases 1 to 1710)		
REFERENCE Duan, G.C. and Dai,L.P.		
REFERENCE Title		
JOURNAL Daxue Road 40th, Zhengzhou, Henan 450052, P.R. China		
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 ORGANISM Campylobacter jejuni  
 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 Campylobacteraceae; Campylobacter.  
 REFERENCE 1. (bases 1 to 1710);  
 AUTHORS Labigne,A.  
 TITLE Nucleotide sequence codings for a protein with urea reactivity  
 JOURNAL Patent: EP 0367644 A 8 09-MAY-1990;  
 INSTITUT PASTEUR  
 FEATURES location/Qualifiers  
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 /organism="Campylobacter jejuni."  
 /mol\_type="unassigned DNA"  
 /ab\_xref="txaxon:197"  
 CDS /codon\_start=1



**LOCUS** A08818  
**DEFINITION** C.Jejuni DNA for 61 kDa protein.  
**ACCESSION** A08818  
**VERSION** A08818.1 GI:412247  
**KEYWORDS**  
**SOURCE** Campylobacter jejuni  
**ORGANISM** Campylobacter jejuni  
**BACTERIA; Proteobacteria; Bsp; epsilonproteobacteria; Campylobacterales;**  
**Campylobacteraceae; Campylobacter.**  
**REFERENCE** 1 (bases 1 to 1710)  
**JOURNAL** Patent: WO 9004030-A 8 19-APR-1990;  
**FEATURES** location/Qualifiers  
**source**  
**1.** 1710  
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**Db 222 AspPhePheGlyThrThrProSerAlaLeuPheGlyLeuSerValAlaAspGlyThrAsp 241**  
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 Job time : 5478.47 Secs

GenCore version 5.1.6  
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Post-processing: Minimum Match 0% Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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5	2244	74.8	2619	2 US-08-467-822-19
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7	2244	74.8	2619	3 US-08-466-248-19
8	2028.5	67.6	6131	1 US-07-732-242-C8
9	1828	61.0	1701	4 US-09-252-991A-10316
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11	1826	60.9	1716	5 PCT-US96-05320A-541
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ALIGNMENTS

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; Patent No. 5837240  
; GENERAL INFORMATION:  
; APPLICANT: Cynthia K. Lee et al.  
; TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/920,095  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/08/431,041  
; FILING DATE: 26-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 06132/013001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 2735 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
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; US-08-920-095-1

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; TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; STATE: Boston  
; COUNTRY: USA

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 COMPUTER READABLE FORM:  
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 OPERATING SYSTEM: PC-DOS/MS-DOS  
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 FILING DATE: 23-APR-1996  
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 FILING DATE: 28-APR-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/568, 122  
 FILING DATE: 06-DEC-1995  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 06132/020001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2735 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 PCT-US96-05800-1

Alignment Scores:  
 Pred. No.: 6.26e-247 Length: 2735  
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 Query Match: 76.59% Indels: 0  
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Db 1668 GCTCTGATATTAACTAGCGGTGAAACACACATCTCCCGCTTCACTAACCC 1727

Qy 302 ThrIleProTyroTyrrIleAsnThrValAlaGluAlaIleAspMetLeuMetThrCysHis 321

Db 1728 ACCITCCCTTCACCGTGTAACTAGAGAAGGACATGACATGGCTTATGGTGGCCAC 1787

Qy 322 HisLeuAspIleValGlyGluGlyAspLeuGlyIutPheSerAlaSerArgIleAspProGly 341

Db 1788 CACTGGATTAAGCATTAAAGAATGATCTGCTGATCAAGGATCCACCCCTCA 1847

Qy 342 SerIleAlaAlaGluAlaValLeuHisAspMetGlyValLeuAlaMetThrSerSerAsp 361

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Qy 362 SerGlnAlaMetGlyArgAlaGlyGluValLeuProArgThrTyrGlnIleAlaAspLys 381

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Qy 382 AspIysLysGluPheGlyLysLeuProGluAspGlyLysAspAsnAspAsnProAspArgLe 401

Db 1968 AACAGAGAAAGATTGGCGCTGTAAGGAGAAAAGGGATACGACACTTCAGGATC 2027

Qy 402 LysArgTyrIleAspLysTyrThrIleAsnProIleLeuLeuIleAlaMetThrHisGlyValSerGlyIutY 421

Db 2028 AAAGCTTCTGCTAAATACACCAATTACCCAGCGAGCTGCTCATGCGATTACGGAGAT 2087

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Db 2088 GTAGCTTCTGCTAGAGTGGCGCAAGTGGCTGACTTGGTATTGCGAGCTCTT 2147

Qy 442 GlyValValAspProIleValIleLysGlyIutYrap 461

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Qy 502 ValIysGluIysLeuGlyIutLeuGluAsnGlyValIleProValValAsnCysSerAsnIle 521





**RESULT 5**  
**US-08-467-822-19**  
**Sequence US/08467822**  
**Patent No. 5843460**  
**GENERAL INFORMATION:**  
**APPLICANT: LaBoigne, Agnes**  
**APPLICANT: Saurobaum, Sébastien**  
**APPLICANT: Ferrero, Richard L.**  
**APPLICANT: Thibierge, Jean-Michel**  
**TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST**  
**TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDE**  
**TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SE**  
**TITLE OF INVENTION: POLYPEPTIDES**  
**NUMBER OF SEQUENCES: 44**  
**CORRESPONDENCE ADDRESS:**  
**ADDRESSEE: Finnean, Henderson, Farabow, Garrett &**  
**ADDRESS: Dunner**  
**STREET: 1300 I Street, N.W.**  
**CITY: Washington**  
**STATE: D.C.**  
**Country: USA**  
**ZIP: 20005-3315**  
**COMPUTER READABLE FORM:**  
**MEDIUM TYPE: Floppy disk**  
**COMPUTER: IBM PC compatible**  
**OPERATING SYSTEM: PC-DOS/MS-DOS**  
**SOFTWARE: Patentin Release #1.0, Version #1.30**  
**CURRENT APPLICATION DATA:**  
**APPLICATION NUMBER: US/08/467,822**  
**FILING DATE: 06-JUN-1995**  
**CLASSIFICATION: 435**  
**PRIOR APPLICATION DATA:**  
**APPLICATION NUMBER: US 08/447,177**  
**FILING DATE: 19-MAY-1995**  
**CLASSIFICATION: 435**  
**PRIOR APPLICATION DATA:**  
**APPLICATION NUMBER: US 08/432,697**  
**FILING DATE: 02-MAY-1995**  
**CLASSIFICATION: 435**  
**ATTORNEY/AGENT INFORMATION:**  
**NAME: May, Kenneth J.**  
**REGISTRATION NUMBER: 25,146**  
**REFERENCE/DOCKET NUMBER: 03495.0137-02000**  
**TELECOMMUNICATION INFORMATION:**  
**TELEPHONE: (202) 408-4400**  
**TELEFAX: (202) 408-4400**  
**INFORMATION FOR SEQ ID NO: 19:**  
**SEQUENCE CHARACTERISTICS:**  
**LENGTH: 2619 base pairs**  
**TYPE: nucleic acid**  
**STRANDEDNESS: double**  
**TOPOLOGY: linear**  
**MOLECULE TYPE: DNA (genomic)**  
**FEATURE:**  
**NAME/KEY: misc feature**  
**LOCATION: 31..36**  
**OTHER INFORMATION: /standard\_name= "Shine-Dalgarno**  
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**OTHER INFORMATION: sequence."**  
**US-08-467-822-19**

Percent Similarity: 85.01%      Conservative: 71  
 Best Local Similarity: 72.49%      Mismatches: 85  
 Query Match: 74.82%      Indels: 0  
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**US-09-994B-3 (1-568) x US-08-467-822-19 (1-2619)**

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Db	892 ATCAATTGTTGGGGGGGTAACATATCCCTGATGGGATggTCAACCATAGCCCTAGC 951	Qy	382 AsnLysLysGluPheGlyLysLeuProGluLysPheGlyAspAsnAspAsnAspPheArgle 401
Qy	62 GluAlaThrLeuAspLeuValIleThrAsnAlaMetIleLeaPtyrThrGlyIleTyr 81	Db	1912 AACAAAAGAGTTGAGGCGCTGAAGAGGAGAAAAGGGAAGCAGAACGACACTCCGATC 1971
Db	952 TCTTATGATTAGATTGTTGGTGCCTACTACGCCCATGTCAGGATATAGGGCATTTAC 1011	Qy	402 LysAspTyrlIleSerLysTyrrHileAspLeuProAlaLeuThrHisGlyValSerGluTr 421
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Qy	222 AspTrpGlyThrThrProSerAlaIleAspHicGlyAspLeuValAlaAspGluTyrap 241	Db	2392 TATAAGGTGAAGTGGATGGCAAGGGATACTCTAAAGGAGCAGATGTTGAGCCTA 2451
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Db	322 HisLeuAspLysArgIleArgGluAspIleGluIlePheSerGlnSerArgIleGlyProGly 341	APPLICANT: Ferrero, Richard L.	
Qy		APPLICANT: Thibierge, Jean-Michel	
Db		TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTON, POLYPEPTIDES FOR USE IN THE	
Qy		TITLE OF INVENTION: COMPOSITIONS, AND NUCLEAR ACID SEQUENCES ENCODING SAID	
Db		TITLE OF INVENTION: POLYPEPTIDES	
Qy		NUMBER OF SEQUENCES: 44	
Db		CORRESPONDENCE ADDRESS:	
Qy		ADRESSEE: Dunner, STREET: 1300 I Street, N.W.	
Db		CITY: Washington STATE: D.C.	
Qy		COUNTRY: USA ZIP: 20005-3315	
Db		COMPUTER READABLE FORM:	

MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentInRelease #1.0, version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/432,697  
 FILING DATE: 02-MAY-1995  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Moyes, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE DOCKET NUMBER: 0395.0137-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4000  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2619 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 31..36  
 OTHER INFORMATION: /standard name= "Shine-Dalgarno  
 OTHER INFORMATION: sequence."  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 756..759  
 OTHER INFORMATION: /standard name= "Shine-Dalgarno  
 OTHER INFORMATION: sequence."  
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 Alignment Scores:  
 Pred. No.: 5.14e-241 Length: 2619  
 Score: 2244.00 Matches: 411  
 Percent Similarity: 85.01% Conservative: 71  
 Best Local Similarity: 72.49% Mismatches: 85  
 Query Match: 74.82% Indels: 0  
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 Qy 402 LysArgTyrosIleSerIysTyThrIleAspProAlaIleThrIleGlyValSerIleGlyTyr 421  
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 Qy 442 GlyValIysProLysIleValIleIleGlyIleGlyMetValValPhoSergIumetGlyAsp 461  
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RESULT 7  
 US-08-466-248-19  
 ; Sequence 19, Application US/08466248  
 ; Patent No. 6228359

GENERAL INFORMATION:  
 APPLICANT: Labigne, Agnes  
 APPLICANT: Sauerbaum, Sébastien  
 APPLICANT: Ferero, Richard L.  
 APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNODIRECTIVE COMPOSITIONS AGAINST HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE TITLE OF INVENTION: COMPOSITIONS, AND NUCLEAR ACID SEQUENCES ENCODING SAID TITLE OF INVENTION: POLYPEPTIDES NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dunner  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3315

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,248  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/447,177  
 FILING DATE: 19-MAY-1995  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/432,697  
 FILING DATE: 02-MAY-1995  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Meyer, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03495.0137-02000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4400  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 19:  
 LENGTH: 2619 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 31..36  
 OTHER INFORMATION: / standard\_name= "Shine-Dalgarno"  
 OTHER INFORMATION: sequence..  
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NAME/KEY: misc feature  
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 OTHER INFORMATION: sequence..

US-08-466-248-19

Alignment Scores:  
 Pred. No.: 5.14e-241 Length: 2619  
 Score: 2244.00 Matches: 411  
 Percent Similarity: 85.01% Conservative: 71  
 Best Local Similarity: 72.49% Mismatches: 85  
 Query Match: 74.82% Indels: 0  
 DB: 3 Gaps: 0

US-09-904-994B-3 (1-568) x US-08-466-248-19 (1-2619)

Qy 2 LysMetLysIysGlnGlnLysValAsnThrTyxGlyProThrLysGlyAspLysValarg 21  
 Db 772 AGATTCACGAAAGAATGTTCTATGCTATGTCCTCACTACGGGAGTCGTTACA 831  
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STATE: New York  
 COUNTRY: USA  
 ZIP: 10016-2088

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 0.7mb  
 COMPUTER: IBM PC compatible (NEC PC-9801 RX)  
 OPERATING SYSTEM: MS DOS  
 SOFTWARE: ASCII FORM

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/732,242C  
 FILING DATE: 19910718  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JPN 2-210178  
 FILING DATE: 10-AUG-1990

ATTORNEY/AGENT INFORMATION:

NAME: Goodman, Herbert  
 REGISTRATION NUMBER: 17081

REFERENCE/DOCKET NUMBER: 910532/HG

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)972-1400  
 TELEFAX: (212)370-1622  
 TELEX: 23628

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 6131 base pairs  
 TYPE: NUCLEAR ACID  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)

US-07-732-242C-8

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Percent Similarity:	Mismatches:	Indels:	Query Match:	DB:
	3.01e-216	6131	375	79.72%	77	3	1	
	2028.50				112			2151

Best Local Similarity: 66.14%  
 Mismatches: 112  
 Indels: 3  
 Gap: 2

QY |||||||GAGGAAACACATTCGACCAATATCGCTTGTGGCAAGCTCGCTGCTT 2091

QY |||||||GAGGAAACACATTCGACCAATATCGCTTGTGGCAAGCTCGCTGCTT 461

Db 462 SerAsnAlaSerValProThrProGlnProValTyryArgLysLeuPheGlyIle 481

Db 2152 GCGAATCGGTCTATCCACCCCTACGCCGCTATTACGGTGAAGAATGTTGACCAT 2211

QY 482 GlyLysAlaPheAspThrSerIleThrPheValSerIleValAlaTyrgluAngly 501

Db 2212 GCGGAAACACATTCGACCAATATCGCTTGTGGCAAGCTCGCTGCTT 2271

QY 502 ValLysGluLysLeuGlyLeuGluArgLysValLeuProValLysSerArgAsnile 521

Db 2272 ATCAAAGAGAACGACTAGGCATGATCGCGGACCGCCAGGAAACTGCGCAATTC 2331

QY 522 ThrlsLysAspPhelysPheAsnAspLysIleAlaLysIleThrValAspProLysThr 541

Db 2332 ACTAAAGAACGCTCAATTCAACGATGTGACGCCAGATATGATGTCACCTGAAACC 2391

QY 542 PheGluValPheValAspGlyLysLeuCystSerIleSerProThrSerGluValProLeu 561

Db 2392 TTAAGGTTGAAGATGCTGGCAAGGCAAGCTCTAAAGCGCAGATGATGAACTCTA 2451

QY 562 AlaGluLysGlyThrPhePhe 568

Db 2452 GCGCAACTTATAATTGTC 2472

RESULT 8

US-07-732-242C-8

; Sequence 8, Application US/07732242C

; Patent No. 5208399

; GENERAL INFORMATION:

; APPLICANT: Uozumi, Takeshi; Masaaki, Haruhiko;

; APPLICANT: Hidaka, Makoto; Nakamura, Akira;

; APPLICANT: Maeda, Michihisa; Yoneta, Yasuo

; TITLE OF INVENTION: Gene of Urease

; NUMBER OF SEQUENCES: 14

; ADDRESSEES: Fritch, Holtz, Goodman & Woodward, P.C.

; STREET: 600 Third Avenue

CITY: New York

QY 162 ProValAspGlyThrAsnAlaThrThrLeuThrProGlyAspTyrAspLeuHisArgMet 181  
Db CCCGTACAGCACAATGCCACTTGTCACGGGGCTTGGAATCCATCGTATG 1522  
QY 182 LeuArgAlaLalaGluGluThrSerMetAsnValGlyPheIleGlyLysGlySerSer 201  
Db 1523 CTTCAAGCAGCCGAGAACTTCCGATAACTTGCTTGTAGGAAGGAACTGTC 1582  
QY 202 SerIysLysGlnLeuValGluGlnValGluAlaGlyAlaLeGlyPheIleLeuHisGlu 221  
Db :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
1583 GATGAGGCTCTTAAGGAACTAACATTGAGGGAGCGTGGGATTAAGCTCACGA 1642  
QY 222 AspTyrGlyThrThrProSerAlaLeuAspGlyAspCysLeuSerValAlaAspGluTyRasp 241  
Db ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
1643 GATGGGGATCCGACCGCGGGCTTGATCATGATGTTGAAGTGGGGATCGATGATG 1702  
QY 242 ValGlnValCysIleHistDraSerThrValAsnGluAlaGlyIleGluGlyAlaLeGlyPheIleLeuHisGlu 261  
Db 1703 GTGCAAGTAGCCGATTCATGACACTTAAATGAGGGGATTTGCGAGGACTTG 1762  
QY 262 AsnAlaMetArgGlyArgAlaLalaHisIleAlaTyrHisIleGluGlyAlaLeGlyPheIleLeuHisGlu 281  
Db 1763 AAGCCATGAGCAGCTGAGCTACATACATACAGAAGGGCTGGCGGAC 1822  
QY 302 ThrIleProTyrrThrIleAsnThrValAlaGluIleAspMetLeuMetThrCysHis 321  
Db ACTCGACCTTATCATCATACTTGGAGAGCATTTGCTGCAC 1942  
QY 322 HisLeuAspIysBargIleArgGluAspLeuGlnPheSerGlnSerArgIleAspGly 341  
Db 1883 CACCTAGAGCTTAATTCGAGGATTTGCTGCAC 1882  
QY 342 SerIleAlaAlaGluAspValLeuHisAspMetGlyValIleAlaMetThrSerSerAsp 361  
Db 2003 ACCATCGCGCGGGAAGATGTTTACATGATTAGCGCTTTCAGCATGTTCTGT 2062  
QY 362 SerCinalaMetGlyArgAlaGlyGluValIleProArgThrTyrGlnThrAlaAspIys 381  
Db 2063 TCAGGGCATGGCGGAGTAGTACATCGTACGGTACAGCTACGAG 2122  
QY 392 AsnIysLysGluPheGlyIysLeuProGluAspGlyIysLeuAspAspIysPheArgIle 401  
Db 2123 ATGAAAAGCAAGGGAAAGTACAGACATGCTCGAGCAACTTCCG 2182  
QY 402 LysArgTyrIleSerIleLysTyrThrIleAsnProAlaLeuThrHisGlyValSerGluThr 421  
Db 2183 AACGTATATGCAATATACATCACTCCGCAATCGGCCATCGCTCTGGGATAT 2242  
QY 422 IleGlySerValGluGluGlyIleAlaAspLeuValProAlaPhePhe 441  
Db :::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
2243 GIGGGCTGCTGAGTGGAAATTAGCTGATTAGCTGGTGTGAACTCTGCTT 2302  
QY 442 GlyIvalLysProIysIleValIleLysGlyGlyMetValValAlpheSerGluMetGlyAsp 461  
Db 2303 GGTGCTGAACTCTGCTTAAAGGAGGATGATGCTACAGACTATGGGACAT 2362  
QY :::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
462 SerAlaSerValProThrProGlnProValTyrTyrArgGluMetPheGlyIleHis 481  
Db 2363 CCCATGCCAGATCCGACACCCGACGGGTTTATCGCCGATGTTGCG 2422  
QY 482 GlyIysAlaIysPheAspThrSerIleLeuThrPheAlaSerIleIleAla 501  
Db :::|||||:|||||:|||||:|||||:|||||:|||||:  
2423 GAGAGTGGCAATACTCACCTCTTGTGAAAGCAGCGTATGAAAGCC 2482  
QY 502 ValIysGluLysIleGluIysGluGlnValLeuProValIysAsnCysArgAsnIle 521  
Db :::|||||:|||||:|||||:|||||:|||||:  
2483 ATTATGAGCAGCTGGTTGAGGAAAGGTGAACCGTCCATGGATTGCGAATG 2542

QY 522 ThrIleGlyAspPheAspAspIysGluAspIysThrAlaLeuThrValAspProLeuThr 541  
Db ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
2543 AGGAAAGATTAATTGAACTAAACCCAAATTGAGTCGATTCAGCA 2602  
QY 542 PheGluValPheValAspGlyIysGluCysThrSerIysProThrSerCinValProLeu 561  
Db :::|||||:|||||:|||||:|||||:  
2603 TAIGRAGTAAAGGATAGACCTCAATTAGTGACATGTGAAACGGCAGAAATCGTCCTATG 2662  
QY 562 AlaGlnArgTyrThrPhePhe 568  
Db ::|||:|||||:  
2663 GCACACGGATTCTTATT 2683

RESULT 9  
US-09-252-991A-10316  
; Sequence 10316 , Application US/09252991A  
; Patent No. 655195  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: ABRUGINDA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107195.136  
; CURRENT APPLICATION NUMBER: US/09/252, 991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074, 788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094, 190  
; CURRENT FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 10316  
; LENGTH: 1701  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
; US-09-252-991A-10316

Alignment Scores:  
Pred. No.: 1.16e-194 Length: 1701  
Score: 1828.00 Matches: 336  
Percent Similarity: 74.47% Conservative: 87  
Best Local Similarity: 59.15% Mismatches: 143  
Query Match: 60.95% Indels: 2  
DB: 4 Gaps: 1

US-09-904-994B-3 (1-568) x US-09-252-991A-10316 (1-1701)

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Db :::|||||:|||||:|||||:  
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QY 21 ArgIleGlyAspThrAspLeuTrpAlaGluValGluHisAspIysTyrThrTyrGlyGlu 40  
Db 61 CGCTGGCGACACCGACCTGIGATCCAGGGAACCTCAGCTCGCTCGGACCGCTG 120  
QY 41 GluIleIysPheGlyIleGlyIysThrIleAspIysGluGlyMetGlyGlnSerAsnSerPro 60  
Db 121 GAAGCTGAACTTCGGGGGGCGAGGTCACTCCGGACGCGATGGCCACAGTCAGTCGGC 180  
QY 61 AspGluAspThrAspIleValIleThrAsnAlaValIleIleAspIysTyrThrGlyIle 80  
Db 181 GCGGGCGACGGGGCGACCGGATCAGCTCGGATCCAGCTCGGCTGATCCTCGACACTGGGCTG 240  
QY 81 TyrIleGlyAspIleGlyIleIysAsnGlyIleValIleIleGlyIleGlyIysAlaGlyIle 100  
Db 241 GTGCAAGGCGACCTGCTCAAGGACCGGGCATCCGGCTCTGGAGGCGGCA 300  
QY 101 LysAspMetGlnAspGlyIysValSerProHisMetValValIlyValGlyIlyValGluAlaIle 120  
Db 301 CCTGACATCCAGCCGGGCTG----ACATGCCATTCGGCCGACCGGAGGTGTC 354  
QY 121 AlaGlyIysGlyIleIleLeuIleAspIysGlyIleAspSerIysThrIleLeuIle 140  
Db 355 GCGCGGAGGGCAGATCTCACGCCGCCGACATCGACACCATCAGTCAGTC 414  
QY 141 ProGlnGlnPheProThrAlaLeuAlaIleGlyIlyValThrThrMetPheGlyGlyIlyThr 160



Alignment Scores:  
PCT-US96-05320A-541  
RESULT 11  
PCT-US96-05320A-541  
Sequence 541, Application PC/TUS9605320A  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences  
APPLICANT: 9410 Key West Avenue  
APPLICANT: Rockville, MD 20850  
APPLICANT: United States of America  
APPLICANT: Johns Hopkins University  
APPLICANT: 720 Rutland Avenue  
APPLICANT: Baltimore, MD 21205  
APPLICANT: United States of America  
APPLICANT: Mark D. Adams  
APPLICANT: Owen White  
APPLICANT: Hamilton O. Smith  
APPLICANT: J. Craig Venter  
TITLE OF INVENTION: Nucleotide sequence of the Haemophilus Influenzae Rd Genome  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSE: Stern, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20003-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/05320A  
FILING DATE: April 12, 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,102  
FILING DATE: June 7, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,429  
FILING DATE: June 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Eric K. Steffe  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488 014PC01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 541:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1716 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
PCT-US96-05320A-541

#### **GENERAL INFORMATION:**

**APPLICANT:** Fleischmann et al.  
**TITLE OF INVENTION:** The Nucleotide sequence

the *Haemophilus influenzae*

NUMBER OF SEQUENCES: 1 Thereof, and uses thereof  
correspondence address.

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue  
CITY: Rockville

STATE: MD  
COUNTRY: USA

COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMMITTEE: DAI BANERJEE

COMPILED: DELL FUSION  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text









Db 1198 ATCCATATAACGTTATCGCTAACATACAGTATCCGCACGGCACATGCCATT 1257  
 Qy 419 SerGluTyrllelgleyservallglugluglylysilealraspleuvalwtrPasnPro 438  
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 Db 1258 GCTCATACGGGGATCAATGAGAAAGGTAACTTGCGGATATCGTCATGGATCCT 1317  
 Qy 439 AlphePhcGlyVallysProlysileVallelysglylolyMetvalValPheserglu 458  
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 Db 1318 GCTTTCCTTGGCTCAAACGGCACTTATCATAAAGGTTGTTGCTTGTGCTTA 1377  
 Qy 459 MetGLYAspSerAsnAlaSerValProThr-ProGlnProValTyrTyrArgGluMetPhe 478  
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 Db 1378 ATGGGGGATTAATCGGCTTATCCAAACCGCAGCCGGTCATTCATCCATGAT 1437  
 Qy 479 GlyHisIgylLysAlaLysPheAspThrSerIleThrPheValSerLysValAlaTyr 498  
 ::||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 1438 GCCTCTTAGGAAAGCCAAATACTAAACCGTCGATCTTATGTCANAAGCGGTATT 1497  
 Qy 499 GluGluGlyVallysGluLysIleGluGluArgGlnValLeuProValLysSerCys 518  
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 Db 1498 GAGGGGGAGTGCAGAAATAATTAGGCTTAAGGCTTATGGCTTGCGCTGGAGGGCTT 1557  
 Qy 519 ArgAsnIleThrIleLysAspPheAsnAspLysIleThrAlaLysIleThrValAsp 538  
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 Db 1558 CGTCATATCGAAAGCTCGATGATCCACATAACTATCTCCATATCGAATTGAT 1617  
 Qy 539 ProLySThrPheGluValPheValAspGlyLysIeuCysThrSerLysProThrSerGln 558  
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 Db 1618 CCAACAACATTCATGTAAAGCGGATGGTACACTGGTTGTGAGGCCAGGCACTGAA 1677  
 Qy 559 ValProLeuAlaGlnArgThr-PhePhe 569  
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 Db 1678 TTACCGATGGCTCAACGCTTATTCCTTATT 1707

Search completed: February 16, 2005, 01:31:21  
 Job time : 2119.33 secs

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GenCore version 5.1.6

**OM protein - protein search, using sw model**

Run on: February 15, 2005, 20:4:30 : Search time 8.53904 Seconds  
 (without alignments)  
 1975.712 Million cell updates/sec

<b>Title:</b>	US-09-904-994B-2
<b>Perfect score:</b>	1181
<b>Scoring table:</b>	BLOSUM62
Gapp 10.0 , Gapext 0.5	
<b>Searched:</b>	513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 324380

Minimum DB seq length: 0  
 Maximum DB seq length: 100

Post-processing: Minimum Match 100%  
 Maximum Match 100%  
 Listing first 45 summaries

**Database :**

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1: Issued_Patents_AA;*
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2: /cgn2_6/podata/1/1aa/5B_COMBO pep:*
3: /cgn2_6/podata/1/1aa/6A_COMBO pep:*
4: /cgn2_6/podata/1/1aa/6B_COMBO pep:*
5: /cgn2_6/podata/1/1aa/PC7US_COMBO pep:*
6: /cgn2_6/podata/1/1aa/backfile1.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

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Result No.	Score	Query Match	Length	DB ID	Description
1	281.5	23.8	100	1	US-08-967-513-3
2	281.5	23.8	100	2	US-08-967-45B-3
3	269.5	22.8	99	1	US-07-732-542C-1
4	261.5	22.1	100	2	US-08-467-822-23
5	261.5	22.1	100	3	US-08-432-657-23
6	261.5	22.1	100	3	US-08-465-248-23
7	250.5	21.2	100	4	US-09-602-777A-18
8	250.5	5.8	40	4	US-09-602-777A-18
9	62	5.2	97	4	US-09-640-211A-973
10	60	5.1	63	4	US-09-248-976A-23427
11	58	4.9	18	4	US-08-945-038-12
12	57	4.8	83	4	US-09-270-767-60797
13	57	4.8	92	4	US-09-513-999C-321
14	57	4.8	100	4	US-09-328-352-7014
15	56.5	4.8	83	4	US-09-248-796A-23863
16	56	4.7	15	3	US-09-091-001-1
17	56	4.7	64	4	US-09-248-796A-23641
18	56	4.7	86	4	US-09-621-976-4833
19	55.5	4.7	100	4	US-09-621-976-7112
20	54.5	4.6	94	4	US-09-270-767-31087
21	54.5	4.6	94	4	US-09-270-767-53304
22	54	4.6	72	4	US-09-540-236-3389
23	54	4.6	45	4	US-09-248-796A-28048
24	53	4.5	82	4	US-09-689-065B-8
25	52	4.4	77	3	US-08-936-165A-311
26	51.5	4.4	65	4	US-09-248-796A-26949
27	51.5	4.4	68	4	US-09-107-433-4410

**ALIGNMENTS**

---

RESULT 1	US-08-967-513-3
Patent No. 5783436	Sequence 3, Appli
GENERAL INFORMATION:	
APPLICANT: Robert P. Hausinger	TITLE OF INVENTION: Mutant Urease and Method
APPLICATION NUMBER: US/08/967,513	TIME OF INVENTION: of Use For Determination
FILING DATE: 11-NOV-1997	NUMBER OF SEQUENCES: 5
CLASSIFICATION: 435	CORRESPONDENCE ADDRESS:
PRIORITY APPLICATION DATA:	ADDRESSEE: Ian C. McLeod
APPLICATION NUMBER: 08/697,645	STREET: 2130 Commons Parkway
FILING DATE: July 26, 1996	CITY: Okemos
ATTORNEY/AGENT INFORMATION:	STATE: Michigan
NAME: Ian C. McLeod	COUNTRY: USA
REGISTRATION NUMBER: 20,931	ZIP: 48864
REFERENCE DOCKET NUMBER: MSU 4.1-309	COMPUTER READABLE FORM:
TELECOMMUNICATION INFORMATION:	MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
TELEPHONE: (517) 347-4100	COMPUTER: IBM Compatible
TELEFAX: (517) 347-4103	OPERATING SYSTEM: MS-DOS
TELEX: No. 5783436e	SOFTWARE: Wordperfect 5.1
INFORMATION FOR SEQ ID NO: 3:	CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:	APPLICATION NUMBER: US/08/967,513
LENGTH: 100	FILING DATE: 11-NOV-1997
TYPE: amino acids	CLASSIFICATION: 435
STRANDEDNESS: Single	PRIORITY APPLICATION DATA:
TOPOLOGY: Linear	APPLICATION NUMBER: 08/697,645
MOLECULE TYPE:	FILING DATE: July 26, 1996
DESCRIPTION: Protein	ATTORNEY/AGENT INFORMATION:
HYPOTHETICAL: No	NAME: Ian C. McLeod
ANTI-SENSE: No	REGISTRATION NUMBER: 20,931
ORIGINAL SOURCE:	REFERENCE DOCKET NUMBER: MSU 4.1-309
ORGANISM: N/A	TELECOMMUNICATION INFORMATION:

```

Sequence 61, Appl
Sequence 8, Appl
Sequence 881, App
Sequence 3479, Ap
Sequence 25293, A
Sequence 10059, A
Sequence 26429, A
Sequence 81, Appl
Sequence 81, Appl
Sequence 6687, Ap
Sequence 112, App
Sequence 3459, Ap
Sequence 5320, Ap
Sequence 38, Appl
Sequence 38, Appl
Sequence 5808, Ap
Sequence 6886, Ap
Sequence 10 (and)

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STRAIN: N/A  
 INDIVIDUAL ISOLATE: N/A  
 CELL TYPE: N/A  
 FEATURE:  
 NAME/KEY: subunit Urea  
 LOCATION:  
 IDENTIFICATION METHOD: Sequencing  
 OTHER INFORMATION: encoded subunit of  
 OTHER INFORMATION: mutant urease

US-08-967-513-3

Query Match

Best Local Similarity 23.8%; Score 281.5; DB 1; Length 100;

Matches 59; Conservative 18; Mismatches 22; Indels 1; Gaps 1;

QY 1 VKLTPKEQEKKFLYLAGEVARRKRAEGLKLNQPEAIAYSAHIMDEARCKKTAQLMEE 60  
 Db 1 MELTPREPKDKULLFRAILVAERRLARGLKUNYPESVALSAPINEGARDG-KSVASLMEE 59

QY 61 CMHFLKIKDEEMPGVGMNPVDLGVEATPDPGTKLVTVNWI 100  
 Db 60 GRHVLTREQQMEGVPEMPIDIOVEATPPDGSKLVTVNPI 99

RESULT 2

US-08-687-645B-3

Sequence 3, Application US/08687645B

Patent No. 5846752

GENERAL INFORMATION:

APPLICANT: Robert P. Hausinger

TITLE OF INVENTION: Mutant Urease and Method

TITLE OF INVENTION: of Use For Determination

TITLE OF INVENTION: of Urea

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ian C. McLeod

STREET: 2190 Commons Parkway

CITY: Okemos

STATE: Michigan

COUNTRY: USA

ZIP: 48864

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,645B

FILING DATE: July 26, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Ian C. McLeod

REGISTRATION NUMBER: 20,931

REFERENCE/DOCKET NUMBER: MSU 4.1-309

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 347-1100

TELEFAX: (517) 347-4103

TELEX: No. 5846752

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 100

TYPE: amino acids

STRANDEDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE:

DESCRIPTION: Protein

HYPOTHETICAL: No

ANTI-SENSE: No

ORIGINAL SOURCE:

ORGANISM: N/A  
 STRAIN: N/A  
 INDIVIDUAL ISOLATE: N/A  
 CELL TYPE: N/A  
 FEATURE:  
 NAME/KEY: subunit Urea  
 LOCATION:  
 IDENTIFICATION METHOD: Sequencing  
 OTHER INFORMATION: encoded subunit of  
 OTHER INFORMATION: mutant urease

US-08-687-645B-3

Query Match

Best Local Similarity 23.8%; Score 281.5; DB 2; Length 100;

Matches 59; Conservative 18; Mismatches 22; Indels 1; Gaps 1;

QY 1 VKLTPKEQEKKFLYLAGEVARRKRAEGLKLNQPEAIYSAHIMDEARCKKTAQLMEE 60  
 Db 1 MELTPREPKDKULLFRAILVAERRLARGLKUNYPESVALSAPINEGARDG-KSVASLMEE 59

QY 61 CMHFLKIKDEEMPGVGMNPVDLGVEATPDPGTKLVTVNWI 100  
 Db 60 GRHVLTREQQMEGVPEMPIDIOVEATPPDGSKLVTVNPI 99

RESULT 3

US-07-732-242C-1

Sequence 1, Application US/0773224C

Patent No. 5298399

GENERAL INFORMATION:

APPLICANT: Uozumi, Takeshi, Masaki, Haruhiko;

APPLICANT: Hidaka, Makoto; Nakamura, Akira;

APPLICANT: Maeda, Michihisa; Yoneta, Yasuo

TITLE OF INVENTION: Gene of Urease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Frishauf, Holtz, Goodman &amp; Woodward, P.C.

STREET: 600 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10016-2088

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 0.72mb

COMPUTER: IBM PC compatible (NEC PC-9801 RX)

OPERATING SYSTEM: MS DOS

SOFTWARE: ASCII Form

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/732,242C

FILING DATE: 19910718

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JPN 2-210178

FILING DATE: 10-AUG-1990

ATTORNEY/AGENT INFORMATION:

NAME: Goodman, Herbert

REGISTRATION NUMBER: 17081

REFERENCE/DOCKET NUMBER: 910532/HG

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)972-1400

TELEFAX: (212)370-1622

TELEX: 236268

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 99 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE:

DESCRIPTION: peptide

HYPOTHETICAL: No

ANTI-SENSE: No

ORIGINAL SOURCE:

Query Match 22.8%; Score 269.5; DB 1; Length 99;  
 Best Local Similarity 55.6%; Pred. No. 9e-23;

Matches 55; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

QY 2 KLTPEKEKFLYYAGEVARRKKGKLUQPEAIAYSAHIMDEARRGKKVQLMEEC 61  
Db 1 KLTSEMEKLMIIVAADLARRKRGKLNYPEAVAMITYVELEGARDG-KTVQLMQY 59

RESULT 4  
US-08-467-822-23  
Sequence 23 Application US/08467822  
Patent No. 584360  
GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastian  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTON, POLYPEPTIDES FOR USE IN THE COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID TITLE OF INVENTION: POLYPEPTIDES NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,822  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,177  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 100 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-432-697-23

Query Match 22.1%; Score 261.5; DB 2; Length 100;  
Best Local Similarity 56.0%; Pred. No. 7.4e-22;  
Matches 56; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

QY 1 VKLTPEKEKFLYYAGEVARRKKGKLUQPEAIAYSAHIMDEARRGKKVQLMEE 60  
Db 1 MELTPREKOKLULTAGLVAAERLAKGKLNYPEAVAMITYVELEGARDG-KTVQLMSE 59

RESULT 5  
US-08-432-697-23  
Sequence 23 Application US/08432697  
Patent No. 6248330  
GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastian  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTON, POLYPEPTIDES FOR USE IN THE COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 100 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-432-697-23

Query Match 22.1%; Score 261.5; DB 3; Length 100;  
Best Local Similarity 56.0%; Pred. No. 7.4e-22;  
Matches 56; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

QY 1 VKLTPEKEKFLYYAGEVARRKKGKLUQPEAIAYSAHIMDEARRGKKVQLMEE 60  
Db 1 CMHFLKKDEVMPGVGNMVPDLGEATFPDGTKLVLVNPPI 100

RESULT 6  
US-08-466-248-23  
Sequence 23 Application US/08466248  
Patent No. 6258359  
GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastian

Query Match 22.1%; Score 261.5; DB 2; Length 100;  
Best Local Similarity 56.0%; Pred. No. 7.4e-22;  
Matches 56; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

QY 1 VKLTPREKOKLULTAGLVAAERLAKGKLNYPEAVAMITYVELEGARDG-KTVQLMSE 60  
Db 1 MELTPREKOKLULTAGLVAAERLAKGKLNYPEAVAMITYVELEGARDG-KTVQLMSE 59

APPLICANT: Ferrero, Richard L.  
 APPLICANT: Thibierge, Jean-Michel  
 TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
 TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
 TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
 NUMBER OF SEQUENCES: 44  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: Flanagan, Henderson, Farabow, Garrett &  
 STREET: 1300 T Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,248  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 FILING DATE: 02-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE DOCKET NUMBER: US 08/432,697  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4000  
 FAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 100 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-466-248-23

Query Match 22.1% Score 261.5; DB 3; Length 100;  
 Best Local Similarity 56.0%; Pred. No. 4e-22; Mismatches 17; Indels 1; Gaps 1;  
 Matches 56; Conservative

Qy 1 VVLTPEQKEKFLIVYAGVARRKAEGLKLNPQEAIYISHAHIMDEARRGKKTVAQLMEE 60  
 Db 1 MELTPREKDKLILLFTAGIWAERRLAKGLKLNPVERVALISCAIMEGAREG-KTVAOLMSE 59

Qy 61 CHFLKLKDVEMPGVGNMVPDLGEATEFPDGTVLKVTVWAPI 100  
 Db 60 GRVVLTAEQVMSCVPEMIKDVQEVCFPDGTKLVSIHSPI 99

US-08-466-248-23

RESULT 7  
 US-09-602-77A-18  
 Sequence 18, Application US/0960277A  
 ; Paten No. 6831165  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pompejus, Markus  
 ; APPLICANT: Kroger, Burkhard  
 ; APPLICANT: Schröder, Hartwig  
 ; APPLICANT: Zölder, Oskar  
 ; APPLICANT: Haberhauer, Gregor  
 TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION

FILE REFERENCE: BGI-128CP  
 CURRENT APPLICATION NUMBER: US/09/602,77A  
 CURRENT FILING DATE: 2000-06-23  
 PRIOR APPLICATION NUMBER: US 60/141031  
 PRIOR FILING DATE: 1999-06-25  
 PRIOR APPLICATION NUMBER: DE 19931636.8  
 PRIOR FILING DATE: 1999-07-08  
 PRIOR FILING DATE: 1999-07-09  
 PRIOR APPLICATION NUMBER: DE 19932125.6  
 PRIOR FILING DATE: 1999-07-09  
 PRIOR APPLICATION NUMBER: DE 19932126.4  
 PRIOR FILING DATE: 1999-07-09  
 PRIOR APPLICATION NUMBER: DE 19932127.2  
 PRIOR FILING DATE: 1999-07-09  
 PRIOR APPLICATION NUMBER: DE 19932128.0  
 PRIOR FILING DATE: 1999-07-10  
 PRIOR APPLICATION NUMBER: DE 19932129.9  
 PRIOR FILING DATE: 1999-07-19  
 PRIOR APPLICATION NUMBER: DE 19932226.0  
 PRIOR FILING DATE: 1999-07-09  
 PRIOR APPLICATION NUMBER: DE 19932920.6  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19932921.9  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19932922.2  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19932924.9  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19932928.1  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19932930.3  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19932933.8  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19932935.4  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19932937.7  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19932938.9  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19933005.0  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19933006.9  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19933007.6  
 PRIOR FILING DATE: 1999-07-14  
 PRIOR APPLICATION NUMBER: DE 19941378.9  
 PRIOR FILING DATE: 1999-08-31  
 PRIOR APPLICATION NUMBER: DE 19941379.7  
 PRIOR FILING DATE: 1999-08-31  
 PRIOR APPLICATION NUMBER: DE 19941390.8  
 PRIOR FILING DATE: 1999-08-31  
 PRIOR APPLICATION NUMBER: DE 19941391.6  
 PRIOR FILING DATE: 1999-08-31  
 PRIOR APPLICATION NUMBER: DE 19942088.2  
 PRIOR FILING DATE: 1999-09-03  
 NUMBER OF SEQ ID NOS: 442  
 SEQ ID NO 18  
 LENGTH: 100  
 TYPE: PRT  
 ORGANISM: Corynebacterium glutamicum  
 US-09-602-77A-18

Query Match 21.2% Score 250.5; DB 4; Length 100;  
 Best Local Similarity 52.0%; Pred. No. 1.3e-20; Mismatches 51; Conservative 20; Indels 1; Gaps 1;  
 Matches 51; Conservative

Qy 3 LTPKEQKEKFLIVYAGVARRKAEGLKLNPQEAIYISHAHIMDEARRGKKTVAQLMEBCM 62  
 Db 3 ITPKEQKEKFLIVYAGVARRKAEGLKLNPQEAIYISHAHIMDEARRGKKTVAQLMEBCM 61

Qy 63 HFLKKDVEMPGVGNMVPDLGEATEFPDGTVLKVTVWAPI 100  
 Db 62 TILTRDQDLEGIPEMPDQIWEATEDFGTKLVTVWAPI 99

RESULT 8  
US-09-602-77A-12  
Sequence 12; Application US/0960277A  
; Patent No. 6831165  
; GENERAL INFORMATION:  
; APPLICANT: Rompejus, Markus  
; APPLICANT: Schroder, Burkhard  
; APPLICANT: Zalder, Oskar  
; APPLICANT: Haberhauer, Gregor  
TITLE OF INVENTION: CORYNBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN HOMOSTASIS AND ADAPTATION  
FILE REFERENCE: BGI-128CP  
CURRENT APPLICATION NUMBER: US/09/602,77A  
CURRENT FILING DATE:  
PRIOR APPLICATION NUMBER: US 60/141031  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: DE 19931636.8  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19932125.6  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932126.4  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932127.2  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932128.0  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932129.9  
PRIOR FILING DATE: 1999-07-19  
PRIOR APPLICATION NUMBER: DE 19932127.2  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932128.0  
PRIOR FILING DATE: 1999-07-14  
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PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19932924.9  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19932928.1  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19932930.3  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19932933.8  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19932935.4  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19932973.7  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19933002.6  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19933003.4  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19933005.0  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19933006.9  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19941378.9  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19941379.7  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19941390.8  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19941391.6  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19942088.2  
PRIOR FILING DATE: 1999-09-03  
NUMBER OF SEQ ID NOS: 442  
SEQ ID NO 12  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-602-77A-12

Query Match 5.1%; Score 60; DB 4; Length 63;  
Best Local Similarity 30.9%; Pred. No. 28; Matches 17; Conservative 9; Mismatches 25; Indels 4; Gaps 2;

RESULT 9  
US-09-640-211A-973  
; Sequence 973; Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Sneek, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
TITLE OF INVENTION: Compositions and Methods for the Modification of Gene Transcription  
FILE REFERENCE: 11000.1021CU  
CURRENT APPLICATION NUMBER: US/09/640,211A  
CURRENT FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 2368  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 973  
LENGTH: 97  
TYPE: PRT  
ORGANISM: Pinus radiata  
US-09-640-211A-973

Query Match 5.2%; Score 62; DB 4; Length 97;  
Best Local Similarity 31.0%; Pred. No. 32; Matches 18; Conservative 14; Mismatches 19; Indels 8; Gaps 3;

Qy 114 GCDKDIE--LNAGKEVTELVNEGPKSLHVGSHPFHEFAANKALKFDERKAYKRLD 169  
Db 39 GCERKVNALNSMGKVSSVEVERQYKAVTVG---YDANKVLK--RVQTKRKAEL 90

RESULT 10  
US-09-248-796A-27427  
; Sequence 27427; Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107195.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
PRIOR APPLICATION NUMBER: DE 19933003.4  
PRIOR FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 27427  
LENGTH: 63  
TYPE: PRT  
ORGANISM: Candida albicans  
US-09-248-796A-27427

Query Match 5.1%; Score 60; DB 4; Length 63;  
Best Local Similarity 30.9%; Pred. No. 28; Matches 17; Conservative 9; Mismatches 25; Indels 4; Gaps 2;

Qy 168 DIPSGNTTRIGAGTCKVQLIPIGGSKVIGMGLVNNTADEHHKKHKLDAKSH 222  
Db 11 DIASSVVSSIGGNKV--ADKLHLGGVGHVG--GVAGGIAQNLLEHKADEDEVREH 61

RESULT 11  
US-09-945-038-12  
; Sequence 12; Application US/09945038



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; Patient No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Bretton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACCINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7014
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-7014

RESULT 15
US-09-248-796A-23863
; Sequence 23863, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196-132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23863
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-23863

Query Match 4.8%; Score 56.5; DB 4; Length 83;
Best local similarity 31.8%; Pred. No. 1.1e-02; Mismatches 19; Indels 3; Gaps 1;
Matches 14; Conservative 8; Sensitive 0;
Qy 122 NACKEVTELEVNBGPKSLHVG --HFHFPEANKALKEDRKEKA 162
Db 4 NQGKEBRIERIKIVAKRPTCWTIGSGKNNENFVFTGHLKUDDEKA 47

Search completed: February 15, 2005, 20:44:31.
Job time : 9.53904 secs

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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: February 15, 2005, 20:41:36 ; Search time 87.6675 Seconds  
(without alignments)

4218.194 Million cell updates/sec

**Title:** US-09-904-9943-2  
**Perfect score:** 1181

**Sequence:** VKLTPKSGEKEFVYIYAGEVA. .... ADDRKHKKALDKAKSHGFIK 226

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Ygapop 10.0 ; Ygapext 0.5  
Fgapop 6.0 ; Fgapext 7.0  
DelOp 6.0 , Delext 7.0

**Searched:** 1202784 seqs, 818138359 residues

**Total number of hits satisfying chosen parameters:** 2405568  
Minimum DB seq length: 0  
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**Post-processing:** Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-O=/cgn2\_1/USPRO/spool/US0904994/runat\_11022005\_145649\_25560/app\_query.fasta\_1.1102  
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-MODE=LOCAL -OUTFORMAT= -NORMEXT -HEAPSIZE=000 -MINLEN=0 -MAXLEN=200000000  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOB=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

**Database :**  
1: issued\_Patents\_NA:\*

1: /cgn2\_6/pidata/1/ina/5A COMB seq: \*  
2: /cgn2\_6/pidata/1/ina/5B COMB seq: \*  
3: /cgn2\_6/pidata/1/ina/6A COMB seq: \*  
4: /cgn2\_6/pidata/1/ina/6B COMB seq: \*  
5: /cgn2\_6/pidata/1/ina/PCTUS COMB seq: \*  
6: /cgn2\_6/pidata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query	Length	DB ID	Description
1	610.5	51.7	2735	2 US-08-920-095-1	Sequence 1, Appl
2	610.5	51.7	2735	5 PCT-US56-05800-1	Sequence 1, Appl
3	610.5	51.7	4824	4 US-09-431-705-1	Sequence 1, Appl
4	610.5	51.7	4824	4 US-09-431-705-19	Sequence 19, Appl
5	572.5	48.5	2619	3 US-08-432-697-19	Sequence 19, Appl
6	572.5	48.5	2619	3 US-08-466-248-19	Sequence 19, Appl
7	572.5	48.5	2619	3 US-08-466-248-19	Sequence 19, Appl
8	494.5	41.9	3475	4 US-09-710-219-4022	Sequence 19, Appl
9	480.5	40.7	5966	4 US-08-956-171E-22	Sequence 22, Appl
C	480.5	40.7	5966	4 US-08-986A-22	Sequence 22, Appl
11	474	40.1	2400	2 US-08-967-533-1	Sequence 1, Appl
12	474	40.1	2400	2 US-08-687-645B-1	Sequence 1, Appl

<p><b>RESULT<sup>1</sup></b> US-08-920-095-1</p> <p>Sequence 1, Application US/08920095 Patent No. 5837240</p> <p><b>GENERAL INFORMATION:</b></p> <p>APPLICANT: Cynthia K. Lee et al.</p> <p>TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE</p> <p>NUMBER OF SEQUENCES: 3</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Fish &amp; Richardson P.C.</p> <p>STREET: 225 Franklin Street</p> <p>CITY: Boston</p> <p>STATE: MA</p> <p>COUNTRY: USA</p> <p>ZIP: 02110-2804</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/920, 095</p> <p>FILING DATE:</p> <p>CLASSIFICATION:</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/431, 041</p> <p>FILING DATE: 28-APR-1995</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Clark, Paul T.</p> <p>REGISTRATION NUMBER: 30, 162</p> <p>REFERENCE/DOCKET NUMBER: 06132/013001</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (617) 542-5070</p> <p>TELEFAX: (617) 542-8906</p> <p>INFORMATION FOR SEQ ID NO: 1:</p> <p>SEQUENCE CHARACTERISTICS:</p>	<p><b>ALIGNMENTS</b></p> <p>C 13 468.5 39.7 6133 1 US-07-732-242-C-8 Sequence 8, Appli</p> <p>C 14 467 39.5 1893121 4 US-07-537-984-1 Sequence 1, Appli</p> <p>C 15 467 39.5 1830121 4 US-07-643-990-A-1 Sequence 1, Appli</p> <p>C 16 445.5 37.7 8729 3 US-09-453-702B-258 Sequence 258, App</p> <p>C 17 445.5 37.7 87563 3 US-09-453-702B-57 Sequence 57, Appli</p> <p>C 18 431.5 36.5 4403765 3 US-07-103-840A-2 Sequence 2, Appli</p> <p>C 19 431.5 36.5 4411529 3 US-09-103-840A-1 Sequence 1, Appli</p> <p>C 20 300.5 24.5 462 4 US-09-543-681A-1913 Sequence 1913, AP</p> <p>C 21 281.5 23.8 312 4 US-09-489-039A-2090 Sequence 2090, AP</p> <p>C 22 267.5 22.7 300 5 PCT-US96-05320A-543 Sequence 543, AP</p> <p>C 23 266.5 22.6 324 4 US-09-543-681A-1929 Sequence 1929, AP</p> <p>C 24 264.5 22.4 399 3 US-09-134-001C-2212 Sequence 2212, AP</p> <p>C 25 261 22.1 438 3 US-09-134-001C-2145 Sequence 2145, AP</p> <p>C 26 251 22.1 609 4 US-09-602-777A-9 Sequence 9, Appli</p> <p>C 27 261 22.1 3164 4 US-09-710-279-3828 Sequence 3828, AP</p> <p>C 28 261 22.1 3234 4 US-09-710-279-3853 Sequence 3853, AP</p> <p>C 29 255.5 21.6 312 4 US-09-32-352-1761 Sequence 1761, AP</p> <p>C 30 250.5 21.2 378 4 US-09-252-991A-10313 Sequence 10313, A</p> <p>C 31 250.5 21.2 423 4 US-09-602-777A-17 Sequence 17, Appli</p> <p>C 32 250.5 21.2 813 4 US-09-252-991A-10547 Sequence 10547, A</p> <p>C 33 250.5 21.2 831 4 US-09-252-991A-10512 Sequence 10512, A</p> <p>C 34 247 20.9 336 4 US-09-710-279-115 Sequence 115, AP</p> <p>C 35 239.5 20.3 360 4 US-09-32-352-1789 Sequence 1789, AP</p> <p>C 36 230.5 19.5 306 4 US-09-601-198-92 Sequence 92, Appli</p> <p>C 37 218 18.5 414 4 US-09-252-991A-10315 Sequence 10315, A</p> <p>C 38 215.5 18.2 375 4 US-09-601-198-91 Sequence 91, Appli</p> <p>C 39 208 17.6 330 4 US-09-489-039A-2095 Sequence 2095, AP</p> <p>C 40 119 10.1 789 4 US-09-252-991A-10654 Sequence 10654, A</p> <p>C 41 117 9.9 220 4 US-09-602-777A-11 Sequence 11, Appli</p> <p>C 42 117 9.9 2259 4 US-09-710-279-078 Sequence 4078, AP</p> <p>C 43 94 8.0 1664976 4 US-08-91-421B-1 Sequence 1, Appli</p> <p>C 44 94 8.0 1664976 4 US-08-692-570-1 Sequence 1, Appli</p> <p>C 45 7.0 1664976 4 US-09-692-570-1 Sequence 1578, AP</p>
--	---



QY 121 LeuasnalaGlyLysgluvalThrgluleugluvalthrAengluglyProlysSerleu 140  
   :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:  
 Db 459 ATCAGCAGAACGCAAAGCCCTTACCGTAGCGAAAGTTAAATGTTGGCAAGACCGGT 518  
 QY 141 HisValGlySerHisPheHisPhePheGluAlaValAlaLeuLysPheAspArglu 160  
   :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:  
 Db 519 CAATCGGCCTCACCTCCATTCTTGAGTGAATGATAGTCAGCTTGACCTGG 578  
 QY 161 LysValGlyLysBargleusPileProserGlyLysValThrLeuArgIleGlyAlaGly 180  
   :::|||||:::|||||:::|||||:::|||||:::|||||:  
 Db 579 AAAACTTGGTAACGCTTACGATGGAGCAGGGTAGAGTTGACCTGGC 638  
 QY 181 GlmrhrArglyLysValGlnleuileProleuglyGlySerlysValIleGlyMetAsn 200  
   :::|||||:::|||||:::|||||:::|||||:::|||||:  
 Db 639 GANGAAAATCCGAGAATGATGACATGGCGTAGAGAACATTTGGATTAA 698  
 QY 201 GlyleuvalAsnAsnilelaArglularghislyshislyAlaLeuAspIysAlaLys 220  
   :::|||||:::|||||:::|||||:  
 Db 699 GCATGGTGTAGACAAGCAGAACGAAAGCAAAAATTGCTTACAGAGCTAA 758  
 QY 221 SerHisGlyPhe 224  
 Db 759 GACGCTGGTTT 770

RESULT 3  
 US-09-431-705-1  
 ; Sequence 1, Application US/09431705  
 ; Patent No. 6585975  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kleanthous, Harold  
 ; APPLICANT: Londono-Arcila, Patricia  
 ; APPLICANT: Freeman, Donna  
 ; TITLE OF INVENTION: use of salmonella vectors for  
 ; CURRENT APPLICATION NUMBER: US/09/431,705  
 ; CURRENT FILING DATE: 1999-11-01  
 ; NUMBER OF SEQ ID NOS: 52  
 ; SOFTWARE: FASTSEQ for Windows version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 4824  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: includes sequences from Helicobacter pylori,  
 ; NAME/KEY: CDS  
 ; LOCATION: (2) ... (31)  
 ; NAME/KEY: CDS  
 ; LOCATION: (41) ... (61)  
 ; NAME/KEY: CDS  
 ; LOCATION: (65) ... (799)  
 ; NAME/KEY: CDS  
 ; LOCATION: (803) ... (2512)  
 ; NAME/KEY: CDS  
 ; LOCATION: (2516) ... (2692)  
 ; NAME/KEY: CDS  
 ; LOCATION: (2696) ... (2896)  
 ; NAME/KEY: CDS  
 ; LOCATION: (2800) ... (3322)  
 ; NAME/KEY: CDS  
 ; LOCATION: (3326) ... (3385)  
 ; NAME/KEY: CDS  
 ; LOCATION: (3389) ... (3406)  
 ; NAME/KEY: CDS  
 ; LOCATION: (3410) ... (3466)  
 ; NAME/KEY: CDS  
 ; LOCATION: (3470) ... (3598)  
 ; NAME/KEY: CDS  
 ; LOCATION: (3602) ... (3661)  
 ; NAME/KEY: CDS  
 ; LOCATION: (3665) ... (3697)  
 ; NAME/KEY: CDS

Alignment Scores:  
 Pred. No.: 2.9e-70 Length: 4824  
 Score: 610.50 Matches: 116  
 Percent Similarity: 71.88% Conservative: 43  
 Best Local Similarity: 52.68% Mismatches: 62  
 Query Match: 51.69% Indels: 1  
 DB: 4 Gaps: 1

US-09-904-994B-2 (1-226) × US-09-431-705-1 (1-4824)

QY 1 VallysleuhrProlysglugluglyPhepeleutyrtyralglyGluValAla 20  
 Db 86 ATGAAACTCACCCCAAAAGKGTAGATAAGTTGATGCTCACTACGCTGAGAAATGCT 145

QY 21 ArglysArglyValAglglyLeuIysLeuArgIysLeuArgIysProgluAlaIleAlaTyros 40  
 Db 146 AAAAACGCCAGAAAAGCATTAAGCTTAACATGTTGAGCTTGAGTGTACTTGTATTG 205

QY 41 AlaHisIleMetAspGluAlaArgArgIlyLysIstIstValAlaGlnIeuMetGluGlu 60  
 Db 206 GCCCTATTTATGGAGAGGAGGAGCTGTTAAAGGATCCGCTGATGATCCGAGA 265

QY 61 CysMethisIpheHelyLysAspGluAlaArgArgIlyLysIstIstValAlaGlnIeuMetGluGlu 60

Db 266 GTGGCTTATGAAAGCATGTTCTCTTAAACCAAGATGATGATGATGATGATCCGATGAA 325

QY 81 LeuGlyValGluAlaThrHeProaspGlyThryIysLeuValTrivAlaAsnTProIle 100  
 Db 326 GTGGCTTATGAAAGCATGTTCTCTTAAACCAAGATGATGATGATGATGATCCGATGAA 385

QY 101 GluProAspGluAlaPheLysAlaGlyGluVallySpheGlyCysAspIysAspIleGlu 120  
 Db 386 GGCGCCTAATGTAATTAGTCCGGTAGTG---TCTTAAATAAAGGAGCATCT 442

Db 121 LeuasnalaGlyLysgluvalThrgluleugluvalthrAengluglyProlysSerleu 140  
 Db 443 ATCAGCAGAACGCAAAGCCCTTACCGTAGCGAAAGTTAAATGTTGGCAAGACCGGT 502

QY 141 HisValGlySerHisPheHisPhePheGluAlaValAlaLeuLysPheAspArglu 160  
 Db 503 CAATCGGCCTCACCTCCATTCTTGAGTGAATGATAGTCAGCTTGACACAGACCGGT 562

QY 161 LysValGlyLysBargleusPileProserGlyLysValThrLeuArgIleGlyAlaGly 180  
 Db 563 AAAACTTGGTAACGCTTACGATGGAGCAGAGGAGGAGGAGCTG 622

QY 181 GlmrhrArglyLysValGlnleuileProleuglyGlySerlysValIleGlyMetAsn 200  
 Db 623 GANGAAAATCCGAGAATGATGACATGGCGTAGAGAACATTTGGATTAA 682

QY 201 GlyleuvalAsnAsnilelaArglularghislyshislyAlaLeuAspIysAlaLys 220  
 Db 683 GCATGGTGTAGACAAGCAGAACGAAAGCAGAAATTGCTTACACAGAGCTAA 742

QY 221 SerHisGlyPhe 224  
 Db 743 GAGGGTGGTTT 754

RESULT 4  
 US-09-431-705-19  
 ; Sequence 19, Application US/09431705  
 ; Patent No. 6585975  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kleanthous, Harold

APPLICANT: Freedman, Donna  
 TITLE OF INVENTION: Use of salmonella vectors for vaccination against helicobacter infection

FILE REFERENCE: 06132/060001  
 CURRENT APPLICATION NUMBER: US/09/431,705  
 CURRENT FILING DATE: 1999-11-01  
 NUMBER OF SEQ ID NOS: 52  
 SEQ ID NO: 19  
 LENGTH: 4824  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION; includes sequences from Helicobacter pylori, OTHER INFORMATION: Salmonella typhimurium, and Escherichia coli  
 NAME/KEY: CDS  
 LOCATION: (3893) .. (3934)  
 NAME/KEY: CDS  
 LOCATION: (3938) .. (4027)  
 NAME/KEY: CDS  
 LOCATION: (4031) .. (4285)  
 NAME/KEY: CDS  
 LOCATION: (4289) .. (4300)  
 NAME/KEY: CDS  
 LOCATION: (4304) .. (4408)  
 NAME/KEY: CDS  
 LOCATION: (4412) .. (4471)  
 NAME/KEY: CDS  
 LOCATION: (4475) .. (4588)  
 NAME/KEY: CDS  
 LOCATION: (4592) .. (4669)  
 NAME/KEY: CDS  
 LOCATION: (4673) .. (4711)  
 NAME/KEY: CDS  
 LOCATION: (4715) .. (4774)  
 NAME/KEY: CDS  
 LOCATION: (4784) .. (4824)

S-09-431-705-19

ALIGNMENT SCORE: 2.9e-70  
 red. No.: 610.50  
 core: 71.88%  
 percent Similarity: 52.68%  
 best Local Similarity: 51.69%  
 query Match: 4  
 B:

Length: 4824  
 Matches: 118  
 Conservative: 43  
 Missmatches: 62  
 Indels: 1  
 Gaps: 1

US-09-904-994B-2 (1-226) x US-09-431-705-19 (1-4824)

1 VallyneuThrProlysGluGlnGluLysPheLeuLeuTerTyrAlaGlyGluValAla 20  
 :::::::::::::::::::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:  
 86 ATGAACTCACCACAAAGAGTAGTTAGATTAAGCTTGATGCTCCACTACGGTGGAAATTGC 145  
 21 ArgLysArgLysAlaGluGlyLeuLysLeuGlnInProGuaAlaAlaTyrIleSer 40  
 :::::::::::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:  
 146 AAAAACGCAAGAAAGAGGATAAGCTTAACTCTAGTAGCTTGATGTTAGT 205  
 41 AlaHisLeuMetAspGluLargArgGlyLysLysThrValAlaGlnLeuMetGluGlu 60  
 206 GCCCATTTATGAGAGGAGCGAGCTGGTAAAGAGCTGCCGCGATGTCAGAGAA 265  
 61 CysMethisPheLeuLysAspGluValMetProGlyValGlyAsnMetValProAsp 80  
 :::::::::::::|||||:::|||||:::|||||:::|||||:::|||||:  
 266 GGGCGCTCTCTTTAACACAGATGATGATGATGATGCGCGAACATGATCCATGA 325  
 81 LeuGlyValGluAlaThrPheProArgGlyThrLysLeuValThrValAsnTrpProle 100  
 :::::::::::::|||||:::|||||:::|||||:::|||||:  
 326 GTGGGGATTGAAGCGATGTTCTGATGGACTAATCTGATACCGTACATCCATT 385  
 101 GluProAspGluLysPheGlyLysLysLysGlyCysAspAspIleGlu 120  
 386 GAGGCCATGGTAATTAGTCTCTGGAGATG---TCTTAAAGAAGGACATCACT 442

RESULT 5  
 US-08-467-822-19  
 ; Sequence 19, Application US/08467822  
 ; Patient No. 5943460  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Labigne, Agnes  
 ; APPLICANT: Sauerbaum, Sébastien  
 ; APPLICANT: Ferrero, Richard L.  
 ; APPLICANT: Thibierge, Jean-Michel  
 ; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
 ; TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAIL  
 ; TITLE OF INVENTION: POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 44  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &  
 ; STREET: 1300 I Street, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,822  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/447,177  
 FILING DATE: 19-MAY-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/432,697  
 FILING DATE: 02-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03495.0137-02000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4400  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 2619 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)

NAME/KEY: misc feature  
 LOCATION: 31..36  
 OTHER INFORMATION: / standard name= "Shine-Dalgarno  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 756..759  
 OTHER INFORMATION: / standard name= "Shine-Dalgarno  
 ; OTHER INFORMATION: sequence.n  
 US-08-467-822-19

Alignment Scores:  
 pred. No.: 1.3e-65 Length: 2619  
 Score: 572.50 Matches: 113  
 percent Similarity: 69.64% Conservative: 43  
 Best Local Similarity: 50.45% Mismatches: 67  
 Query Match: 48.48% Indels: 1  
 DB: 2 Gaps: 1

US-09-904-994B-2 (1-226) x US-08-467-822-19 (1-2619)

Qy 1 ValIysLeuthrProLyGluGlnGluLysPheLeuLeuTyTyrAlaGlyIluValAla 20  
 Db 43 ATGAAACTAACGCCCTAAAGACATGAGCACTTAATGCCCATTATGGCCATTGCA 102  
 Qy 21 ArgLySargLysIlaGluGluLysLeuAsnDnPrgLilaLeuAlaTyrIleSer 40  
 Db 103 GAAGAACCGCTTGCCGCGTGGCTGAACTCAATTACACCGAAGCGGTGCGCTCATAGC 162  
 Qy 41 AAlHAlMetIapGluAlaTaGArgIlyLysIstValAlaGlnLeuMetGluGlu 60  
 Db 163 GGGCGTGATGGAAAGCGCGGTGATGCTGTTGAGTCAGCA 222  
 Qy 61 CysMetHisPheIleUlyLysIapGluValMetProGlyValIgLyAsnMetValProIspB 80  
 Db 223 GCAGGAGCTTGCGTTAAAGAAATGATGACGCGCTTGACAGCATGATCAGAA 282  
 Qy 81 LeuGlyValGluAlaThrPheProAspGlyThrIleLeuValThrValAsnTrpProIle 100  
 Db 283 GTCGGGATTGAGCTTACTCCCGATGGAACCAAGCTGTGACTATCCACACTCCGGAA 342  
 101 GuProaspGlnIisPheIysAlaGluLysIapGlyAspIlysAspIleIlu 120  
 Qy 343 GAGGATAATGGCAATATGCCCGGGAGGTc--TCTTAAATGAGGACATTACT 399  
 121 LeuAlaAlaGlyIysIgluValThrGluIleGluValThrAsnGluGlyProIysSerIeu 140  
 400 ATTAAACSCCGGCAAGAGCCATTAGCTGAAATGAGTCCGATCTCCGTG 459  
 Db 460 CAGCTGGGCTCACCTCCACTCTCGAAGTGATAAGCTCTGGACTTCGATGCCA 519  
 Qy 161 IysAlaTyrGlyIysArgLeuAspIleProSerGlyAnthrIleAspIleGlyIly 180  
 Db 520 AAAGCTTGTGCAACGCCATGACATGCTGGAACAGCGGCGCTTGACCCGG 579  
 181 GluThrArgLysValGlnIleIleProLeuGlyIlySerLysIlyValIleGlyMetAsn 200  
 Db 580 GAGGAAAGCTGGAATGAACTCTGACTCTGACATCGGGATAAAGCACTATGCTTAA 639  
 Qy 201 GlyLeuValAsnAlaAlaAspIgluArgIlyIlyIlyAlaLeuAspIlysAlaIys 220  
 Db 640 TCTTGCGGATGCCAAGGCCATGCCATGTTAAACCGCTTAAACCGCTAA 699  
 Qy 221 SerHisGlyPhe 224  
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Db 700 GAAAAGGTTTT 711

RESULT 6  
 US-08-432-697-19  
 ; Sequence 19 Application US/08432697  
 ; Patent No. 6248330  
 GENERAL INFORMATION:  
 APPLICANT: Labine, Agnes  
 APPLICANT: Sauerbaum, Sebastien  
 APPLICANT: Ferraro, Richard L.  
 APPLICANT: Thibierge, Jean-Michel  
 TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
 TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
 TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
 TITLE OF INVENTION: POLYPEPTIDES  
 NUMBER OF SEQUENCES: 44  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/432,697  
 FILING DATE: 02-MAY-1995  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03495.0137-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-4400  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2619 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 31..36  
 OTHER INFORMATION: / standard name= "Shine-Dalgarno  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 756..759  
 OTHER INFORMATION: / standard name= "Shine-Dalgarno  
 ; OTHER INFORMATION: sequence.n  
 US-08-432-697-19

Alignment Scores:  
 Pred. No.: 1.3e-65 Length: 2619  
 Score: 572.50 Matches: 113  
 Percent Similarity: 69.64% Conservative: 43  
 Best Local Similarity: 50.45% Mismatches: 67  
 Query Match: 48.48% Indels: 1  
 DB: 3 Gaps: 1

US-09-904-994B-2 (1-226) x US-08-432-697-19 (1-2619)

Qy 1 ValIysLeuthrProLyGluGlnGluLysPheLeuLeuTyTyrAlaGlyIluValAla 20  
 Db 43 ATGAAACTAACGCCCTAAAGACATGAGCACTTAATGCCCATTATGGCCATTGCA 102

QY 21 ArglyArglyValgluAlaGluGlyLeuIysLeuAngInProgluAlaLeaLtyrIleSer 40  
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 Db 103 GAGAACGCTTGGCCGCTGGTGAACTCATTACCGAGCGCTCGGCCATAG 162  
 QY 41 AlahisilemetAspGluAlaArgArgGlyLeuIysLeuThrValAlaGlnLeuMetGluGlu 60  
 Db 163 GGGCGTGTGAGTGAAGGGGGTGTGGATAAAGCGGTTGCAATGCGAA 222  
 QY 61 CysMetHisPheLeuIysAspGluValMetProGlyValGlyAsnMetValProAsp 80  
 Db 223 GCGAGGACTTCGCTTAAAGAAAATGTTGAGGACCGCGTGTGCAAGCATGATCATGAA 282  
 QY 81 LeuGlyValGluAlaThrPheProAspGlyThrIysLeuValThrValAsnTrpProle 100  
   :::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 283 GTGGGATTGAGCTACTTCCCAGTGAAGCTCGGTAA 342  
 QY 101 GluProAspGluLysPheLeuAlaGlyGluValLeuIysPheGlyCysAspAspIleGlu 120  
 Db 343 GGGATAATGCCAATTAGCCCCGGGGAGTC--TTCTTAATGAGGACATTACT 399  
 QY 121 LeuAsnAlaGlyLysGluValThrGluLeuIysValThrAsnGluGlyProLyserLeu 140  
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 Db 400 ATTAACGCCGGAAGGCACTTAGCTGAAGTAAAGGATCTGGCTGTG 459  
 QY 141 HisValGlySrhIshPhePhePheGluAlaAsnLysAlaLeuIysPheAspArgIle 160  
   :::|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 460 CAGGTGGATCACATTCCACTCTCTGAAAGTAAGCTTCAGCTCGCA 519  
 QY 161 LysAlaTyryGlyLysArgLeuAspIleProSerGlyAsnThrLeuArgIleGlyAlaGly 180  
   :::|||:|||:|||:|||:|||:|||:|||:  
 Db 520 AAAGCTTGGAAACCTGACATGCACTGGACACGGGGCGCTTAACCGGG 579  
 QY 181 GluThrArglyValGlnLeuIleProLeuGlyGlySerIysValIleGlyMetAsn 200  
   :::|||:|||:|||:|||:|||:|||:  
 Db 580 GAGGAAGAAAGTGTGAACTCATGACATCGGGGATAAGGCATCTATGCTTAAT 639  
 QY 201 GlyLeuValAsnAsnIeLeaLaaPgluArgIleLysIshIysValLeuAspIleAlaLys 220  
 Db 640 TCTTGGTGGATGCCAAGGCCATGCCGATGCCGTTAAACGGCTAA 699  
 QY 221 SerHisGlyPhe 224  
 Db 700 GAAAAGGTT; 711

RESULT 7

US-08-466-248-19

; Sequence 19, Application US/08466248

; Patent No. 6258359

; GENERAL INFORMATION:

  APPLICANT: Labigne, Agnes

  APPLICANT: Sauerbaum, Sébastien

  APPLICANT: Ferrero, Richard L.

  APPLICANT: Thibierge, Jean-Michel

  TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE TREATMENT OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID NUMBER OF INVENTION: 44

  CORRESPONDENCE ADDRESS:

    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & STREET: 1300 I Street, N.W.  
     CITY: Washington  
     STATE: D.C.  
     COUNTRY: U.S.A.  
     ZIP: 20005-3315

  COMPUTER READABLE FORM:

    MEDIUM TYPE: Floppy disk

    COMPUTER: IBM PC compatible

    OPERATING SYSTEM: PC-DOS/MS-DOS

    SOFTWARE: Patentin Release #1.0, Version #1.30

    CURRENT APPLICATION DATA:

      APPLICATION NUMBER: US/08/466, 248

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/447,177

FILING DATE: 19-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/432, 697

FILING DATE: 02-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25, 146

REFERENCE/DOCKET NUMBER: 03495. 0137- 02000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4400

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 2619 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: misc. feature

LOCATION: 31..36

OTHER INFORMATION: /standard name= "Shine-Dalgarno

FEATURE:

NAME/KEY: misc. feature

LOCATION: 756..759

OTHER INFORMATION: /standard name= "Shine-Dalgarno

FEATURE:

NAME/KEY: misc. feature

LOCATION: 50..54

OTHER INFORMATION: sequence.π

US-08-466-248-19

Alignment Scores:

Pred. No.: 572.50

Score: 69.64%

Percent Similarity: 50.45%

Best Local Similarity: 48.48%

Query Match: 3

DB: Gaps: 1

Length: 2619

Matches: 113

Conservative: 43

Mismatches: 67

Indels: 1

US-09-904-994B-2 (1-226) x US-08-466-248-19 (1-2619)

QY 1 ValIysLeuThrProLyGluGlnIysPheLeuLeuItyrTyraAlaGlyGluValAla 20  
   :::|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 43 ATGAACTAACGCCCTAAAGAACTAGAACGAACTTAATGCTCATTATGCCGCGCAGTGGCA 102  
 QY 21 ArglyArglyValAlaArgGlyLeuIysLeuAngInProgluAlaLeaLtyrIleSer 40  
 Db 103 GAAGAACGCTTGGCGGTGGTGAACATCAATTACACCGAGGGTCGGCTCATAG 162  
 QY 41 AlahisilemetAspGluAlaArgArgGlyLeuIysLeuThrValAlaGlnLeuMetGluGlu 60  
 Db 163 GGGCGTGTGATGAGAAAGGGCGCGTGTGAATAGCGCTGGCGATTTGATGCGAA 222  
 QY 61 CysMetHisPheLeuIysAspGluValMetProGlyValGlyAsnMetValProAsp 80  
 Db 223 GGCAGGACTTCGCTTAAAGAAAATGTTGAGGCTAGCGATGAGCAGTGTGAA 282  
 QY 81 LeuGlyValGluAlaThrPheProAspGlyThrIysLeuValThrValAsnTrpProle 100  
   :::|||:|||:|||:|||:|||:|||:  
 Db 283 GTGGGATTGAGCTACTTCCCAGTGAACGACTCATCACCGTAA 342  
 QY 101 GluProAspGluLysPheLeuAlaGlyGluValLeuIysPheGlyCysAspIleGlu 120  
 Db 343 GGGATAATGCCAATTAGCCCCGGGGAGTC--TTCTTAATGAGGACATTCT 399  
 QY 121 LeuAsnAlaGlyLysGluValThrGluLeuIysValThrAsnGluGlyProLyserLeu 140  
 Db 400 ATTAACGCCGCAAAGGCCATTAGCTGAAGAATAAAAGGCATGTCCTGTG 459

QY 141 HisValGly-SerHisPheIlePheHeGluAlaLysAlaLeuLysPheAspArgGlu 160

Db 460 CAGGGGATCACATTCACTCTCGAAGTGAATAAGCTCTGACTCGATGCCA 519

QY 161 LysAlaTyroGlyLysBargLeuAspIleProSerGlyAsnThrLeuArgIleGlyAlaGly 180

Db 520 AAAACCTTGCAAAAGCCTAGACTTGCACTCGAACAGGGTCGGCTTA 579

QY 181 GluPheArgLysValGlnLeuIleProLeuGlyGlySerLysValGlyMetAla 220

Db 640 TCTTGGTGGATCCGCAAGCGATCCGATGCTAAACCTGGCTTAACCGCTAA 699

QY 580 GAGGAAAAGTGTGAACTCATCACATGGCGGAAATAGCGSACATCATGGCTTA 639

QY 221 SerHisGlyPhe 224

Db 700 GAAAGAGGTTT 711

**RESULT 8**

US-09-710-279-4032

; Sequence 4032, Application US/09710279

; Patent No. 6701492

; GENERAL INFORMATION:

; APPLICANT: KIMMEL, WILLIAM JOHN

; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTBINS

; FILE REFERENCE: PU3480US

; CURRENT APPLICATION NUMBER: US/09/710,279

; PRIORITY DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 4412

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4032

; LENGTH: 3475

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: nucleic acid sequence

; US-09-710-279-4032

Alignment Scores:

Pred. No. :	4.96e-55	Length:	3475
Score:	494.50	Matches:	109
Percent Similarity:	64.41%	Conservative:	34
Best Local Similarity:	49.10%	Mismatches:	63
Query Match:	41.87%	Indels:	16
DB:	4	Gaps:	4

US-09-904-994B-2 (1-226) x US-09-710-279-4032 (1-3475)

QY 4 ThrProLysGluGlyLysPheLeuIleTyroAlaGlyGluValAlaArgLyBarg 23

Db 1864 ACACACGGAACAGACAACTGGATGATGATGATGCTGAGCTGAGGTGAC 1923

QY 24 LysAlaGluGlyIleLysLeuAspGlnProGluAlaLeuAlaTyrosSerAlaHisIle 43

Db 1924 AAAGCAGAGGACTTTAACCTTAACTTAACTCTGAGCACTGCTTATCGTGTGAAATA 1983

QY 44 MetAspGluLysArgGlyLysThrValAlaGlnLeuMetGluGluCysMetHis 63

Db 1984 TTAGAGGCGGCCTGATGCT---AAACGGTAGCTGACTCATGAGCTTGGAAACA 2040

QY 64 PheLeuLysAlaPheAspGlyThrIleLeuValThrValAsnTrpProLe----- 100

Db 2101 GAAGCCACTTTCCGATGCTAACGCTAACATGCCAACATGTTTAAGCA 2160

QY 101 -----Glu-ProAspGluLysPheLeuAlaGlyGluValAspPheGlyCys 116

Db 2161 GGCATATCATGATCTCTGGAATTT-----GTTAA-----AA 2199

QY 116 PheAspIleGluLeuAsnAlaGlyLysGluValThrGluLeuValThrAsnGluL 136

Db 2200 TACTGAAATGAGCTCAACATCATCCGAAACGGTGTGATGTTGAGTAAATAACGG 2259

QY 136 YProLysSerLeuIleValGlySerLysSerHisPheIlePheGluAlaLysAla 156

Db 2260 CGATAGACCTATACAGTACATTCACATGCGCAATAGCGSACATCATGGCTTA 2319

QY 156 SpheAspArgGluLysAlaTyroGlyLysArgLeuAspIleProSerGlyAsnThrLeuR 176

Db 2320 ATTGATCTGAGAAAGCTATGCTAACATGATGATTCCTCGAGGCTGAGTG 2379

QY 176 GileGlyIaIaGlyIleIhrArgLysValGlnLeuIleProLeuGlyGlySerLysVa 196

Db 2380 ATTGAACTCTGAGATGAAAGAATCTGCAATATTCTGACGAGCTAAAT 2439

QY 196 1IleglyMetAsnIleLeuValAlaAspGluIaGlyLysAla 216

Db 2440 TATCGATTCGCGCTGTTAGCTGATGGCATTATGACGAGAACGGTATTGGTCCAA 2499

QY 216 uASp 217

Db 2500 TGAT 2503

**RESULT 9**

US-09-956-171E-22/C

; Sequence 22, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunisch

; Michael R. Fannon

; Gil H. Choi

; Patrick S. Dillon

; Steven C. Barash

; Craig A. Rosen

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEER: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

COMPUTER TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 485/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: P2248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-2224

TELEFAX: (301) 305-8439

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 5966 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-08-956-171E-22

Alignment Scores:  
Pred. No.: 8.4e-53  
Score: 40.50  
Percent Similarity: 63.35%  
Best Local Similarity: 45.70%  
Query Match: 40.69%  
DB: 4 Gaps: 3

Length: 5966  
Matches: 101  
Conservative: 39  
Mismatches: 69  
Indels: 12

US-09-904-994B-2 (1-226) x US-08-956-171E-22 (1-5966)

QY : 4 ThrProLybGluGlnGluLysPheLeuLeuTyrTyrAlaGlyGluValAlaArgyBarg 23  
Db 4003 ACACAACAGAGAGAGAACAAATTAAATGATGTTGAGTGCGGGCCGAGTGCAGTCGTCTGT 3944  
QY : 24 LysAlaGluGlyLeuLysLeuLysGlnProGluAlaLeaLaTyriReserAlaHisile 43  
Db 3943 AAAGCACGCTGGTTGAACTAAATCATCCTGAGGCAATTAGCTGAATCAGGATGATTA 3884  
QY : 44 MetAspGluAlaArgArgGlyLysThrValAlaGlnLeuMetGluGluCysMethis 63  
Db 3883 TTAGAAGCTGCAAGCAGCTGT---AAGACGTTGCAAGTAAATGAGTTAGCTGAGCAA 3827  
QY : 64 PheLeuLysLysAspGluValMetProGlyValGlyAsnMetValProAspLeuGlyVal 83  
Db 3826 ATTCTAAACAAGAAGATGTCATGAGGTTAACTACAGTACATCACCCCTATG 3767  
QY : 84 GluAlaThrPheProAspGlyThrIleuValThrValAsnTrpPro-IleGluProAs 103  
Db 3766 GAGGCTAGTTGCCGATGTTACTAGTTAACTACAGTACATCACCCCTATG 3715  
QY : 103 pgLuHiPheLysAlaGlyLysGluValIleuValThrValAsnTrpPro-IleGluProAs 103  
Db 3714 ----TTAAAGGAGGCGACTCAATGATACTACAGGAGAAATTACAAAGTAGACAA 3662  
QY : 118 pIeGluLeuAsnAlaGlyLysGluValThrGluLeuGluValThrAsnGluGlyProly 138  
Db 3661 GGTGGAATTAACTACATCCTGAAACACTATGAAACTGTTGAAATACGGAGATCG 3602  
QY : 138 sSerLeuHiValGlySerHiPheHiSHeHeGluAlaAsnLysAlaLeuLysPheAs 158  
Db 3601 ACCAAATTCAAGCTGGCTCACATTTCATTTAGATTAATCCAGCTGAGCAATTGAGATTGCA 3542  
QY : 158 pArgGluLysAlaTyrglyLysArgLeuAspLeuProSerGlyAsnThrLeuArgIegl 178  
Db 3541 AGCTGAAATGGGATATGGAAACATTTAGATTAATCCAGCTGAGCAATTGAGATTGCA 3482  
QY : 178 ValAlaGlyLeuLysArgLysValGlnLeuLeuLysLeuLysLeuValIleGlySerLysLeuValIleGly 198  
Db 3481 ACTGGGGATAAAAAAGAGTCATGTTGATGTTGAACTGCAACGTAATTTTG 3422  
QY : 198 yMetAsnGlyLeuValAsnAsnIleAlaAspGluLysArgHiSlysHiLysAlaLeuLeuAspLy 218  
Db 3421 TTTGGGGTATGGCTCAATGGCTATGATGAGTCAGCTGCTATGCCCACTGTGA 3362  
QY : 218 S 218  
Db 3361 A 3361

RESULT 10

US-08-781-986A-22/C  
Sequence 22, Application US/08781986A  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:

---

ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Disquette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PB248PP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5966 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-22

Alignment Scores:  
Pred. No.: 8.4e-53  
Score: 40.50  
Percent Similarity: 63.35%  
Best Local Similarity: 45.70%  
Query Match: 40.69%  
DB: 4 Gaps: 3

Length: 5966  
Matches: 101  
Conservative: 39  
Mismatches: 69  
Indels: 12

US-09-904-994B-2 (1-226) x US-08-781-986A-22 (1-5966)

QY : 4 ThrProLybGluGlnGluLysPheLeuLeuTyrTyrAlaGlyGluValAlaArgyBarg 23  
Db 4003 ACACAACAGAGAGAACAAATTAAATGATGTTGAGTGCGGGCCGAGTGCAGTCGTCTGT 3944  
QY : 24 LysAlaGluGlyLeuLysLeuLysGlnProGluAlaLeaLaTyriReserAlaHisile 43  
Db 3943 AAAGCACGCTGGTTGAACTAAATCATCCTGAGGCAATTAGCTGAATCAGGATGATTA 3884  
QY : 44 MetAspGluAlaArgArgGlyLysThrValAlaGlnLeuMetGluGluCysMethis 63  
Db 3883 TTAGAAGCTGCAAGTAACTACAGTACATCACCCCTATG 3767  
QY : 84 GluAlaThrPheProAspGlyThrIleuValThrValAsnTrpPro-IleGluProAs 103  
Db 3766 GAGGCTAGTTGCCGATGTTACTAGTTAACTACAGTACATCACCCCTATG 3715  
QY : 103 pgLuHiPheLysAlaGlyLysGluValIleuValThrAsnGluGlyProly 138  
Db 3714 ----TTAAAGGAGGCAATTGATCAGGAGAAATTACAAAGAGCA 3662  
QY : 118 pIeGluLeuAsnAlaGlyLysGluValThrGluLeuGluValThrAsnGluGlyProly 138  
Db 3661 GGTGGAATTAACTACATCCTGAAACAGTTATGAGCTGAAATTACAGGAGATCG 3602  
QY : 138 sSerLeuHiValGlySerHiPheHiSHeHeGluAlaAsnLysAlaLeuLysPheAs 158

NAME/KEY: 'H219Q  
 LOCATION: Modification at position 1312 to  
 LOCATION: Glutamine  
 IDENTIFICATION METHOD: Sequencing  
 OTHER INFORMATION:  
 US-08-967-513-1

Alignment Scores:  
 Pred. No.: 1.56-52 Length: 2400  
 Score: 474.00 Matches: 103  
 Percent Similarity: 64.76% Conservative: 33  
 Best Local Similarity: 49.05% Mismatches: 58  
 Query Match: 40.14% Indels: 16  
 DB: Gaps: 4

RESULT 11  
 US-08-967-513-1  
 Sequence 1, Application US/08967513  
 Patent No. 5783436

GENERAL INFORMATION:  
 APPLICANT: Robert P. Hausinger  
 TITLE OF INVENTION: Mutant Urease and Method  
 TITLE OF INVENTION: of Use For Determination  
 TIME OF INVENTION: of Urea  
 NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ian C. McLeod  
 STREET: 2190 Commons Parkway  
 CITY: Okemos  
 STATE: Michigan  
 COUNTRY: USA  
 ZIP: 48864

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/967,513  
 FILING DATE: 11-NOV-1997  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 REFERENCE/DOCKET NUMBER: MSU 4.1-309  
 APPLICATION NUMBER: 08/687, 645  
 FILING DATE: JULY 25, 1996

ATTORNEY/AGENT INFORMATION:  
 NAME: Ian C. McLeod

REGISTRATION NUMBER: 20, 931

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (517) 347-4100  
 TELEFAX: (517) 347-103  
 TELEX: NO. 5783436

SEQUENCE CHARACTERISTICS:  
 LENGTH: 2400  
 TYPE: nucleotides  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: DNA  
 DESCRIPTION: cDNA  
 HYPOTHETICAL: No  
 ANTI-SENSE: No  
 ORIGINAL SOURCE:  
 ORGANISM: Klebsiella aerogenes  
 STRAIN: CG253  
 INDIVIDUAL ISOLATE:  
 CELL TYPE: N/A  
 FEATURE:  
 NAME/KEY: cDNA encoding mutant urease

---

RESULT 12  
 US-08-687-645B-1  
 Sequence 1, Application US/08687645B  
 Patent No. 5846752

GENERAL INFORMATION:  
 APPLICANT: Robert P. Hausinger  
 TITLE OF INVENTION: Mutant Urease and Method  
 TITLE OF INVENTION: of Use For Determination  
 TIME OF INVENTION: of Urea  
 NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ian C. McLeod

---

RESULT 13  
 US-08-967-513-1  
 Sequence 1, Application US/08967513  
 Patent No. 5783436

GENERAL INFORMATION:  
 APPLICANT: Robert P. Hausinger  
 TITLE OF INVENTION: Mutant Urease and Method  
 TITLE OF INVENTION: of Use For Determination  
 TIME OF INVENTION: of Urea  
 NUMBER OF SEQUENCES: 5

NAME/KEY: 'H219Q  
 LOCATION: Modification at position 1312 to  
 LOCATION: Glutamine  
 IDENTIFICATION METHOD: Sequencing  
 OTHER INFORMATION:  
 US-08-967-513-1

Alignment Scores:  
 Pred. No.: 1.56-52 Length: 2400  
 Score: 474.00 Matches: 103  
 Percent Similarity: 64.76% Conservative: 33  
 Best Local Similarity: 49.05% Mismatches: 58  
 Query Match: 40.14% Indels: 16  
 DB: Gaps: 4

RESULT 14  
 US-09-904-994B-2 (1-226) x US-08-967-513-1 (1-2400)  
 Query 1 ValylsleuthrProlycGluGlnGlyLysPheLeutauTyrralAgl-gluVala 20  
 DB 31 ATGAACTGACCCCGGAAAGAACAGCTTGCCTTACCGCCGCCGGCG 90  
 Query 21 ArglysArglysAlaGluGlyLeuLysLeuAsnGlnProGluAlaLeuAlaTyrlsSer 40  
 DB 91 GAGCTCCGCTGGCCGCGCTGAGCTACATGGAGCGCGCCGTCAGC 150  
 Query 41 AlanisIleMetaaGluAlaArgGlyLysLysThrValAlaGluIleAlaTyrlsSer 60  
 DB 151 GCCTTTATGGAAAGGCCGCTCGGACGCC--AAAAGGTGCGCTCTGATGGAGGA 207  
 Query 61 CysmetHsPheLysLysArgPheLysValMetProGlyValGlyAlaMetValProGly 80  
 DB 208 GGCCTCACTCTGACCCGGAGCAGTGAGGAGCGCTGAGCGCTGCCGGCG 267  
 Query 81 LeuGlyValGluAlaThrPheProAspGlyThrLysLeuValThrValAlaLysTrProlle 100  
 DB 269 ATCCAGGCTGAGCACCTTCCCGACGCTGAGCGCTGAGCGCTGCCGGTACACCCGGTT 327  
 DB 101 -----GluProAspIlu--HisPheLysAlaGlyLysLysValThrGluAla 113  
 DB 328 ATCTGAGGTAGCGCCATATCCCCTGCTATATCACGTTAACGCCGGCAG----- 378  
 Query 114 GlyCysArgLysArgPheAspGlyLysLysLeuValAlaGluValThrGluAla 133  
 DB 379 -----ATGCCCTGAAATCCGCGACCGGAAACCTGTGCTGCGTGGTGTGAG 423  
 Query 134 AsnGluGlyProlysSerIleUhiValGlySerIlePheHisPhePheGluAlaLys 153  
 DB 424 AACCCGCGATCGCCGATTCAGGCTGCTCCACGCTAACCTTGCGGAGGTAACCG 483  
 Query 154 AlanisIlePheAspArgPheLysAlaArgGlyLysArgLysLeuAspIleProserGlyAsn 173  
 DB 484 GCGCTGAACTTCGACCGCTGAGCAGGCCGCGCTATCCCTGATAATCCGGGGCGACG 543  
 Query 174 ThrLeuAspIleGlyAlaGlyGlnThrArgLysValAlaLeuProLeuGlyLys 193  
 DB 544 GCGCTTACGCTTGAACCCGCCAGAAACGCCGACTGAGCTGAGCTGACCTTCGCGGTAC 603  
 Query 194 LysLysValleGlyMetAspGlyLeuVal 203  
 DB 604 CGCCCGCTTCGCTGCGCGCGTC 633

STREET: Okemos Commons Parkway  
 STATE: Michigan  
 COUNTRY: USA  
 ZIP: 48864  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/687, 645B  
 FILING DATE: JULY 26, 1996  
 CLASSIFICATION: 435  
 REFERENCE NUMBER: 100  
 PRIORITY APPLICATION DATA:  
 TELEPHONE: (517) 347-4100  
 TELEX: NO. 5846752e  
 INFORMATION FOR SEQ ID NO: 1:  
 LENGTH: 2400  
 TYPE: nucleotides  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MOLECULE TYPE:  
 DESCRIPTION: cDNA  
 HYPOTHETICAL: No  
 ANTI-SENSE: No  
 ORIGINAL SOURCE:  
 ORGANISM: Klebsiella aerogenes  
 STRAIN: CG253  
 INDIVIDUAL ISOLATE:  
 CELL TYPE: N/A  
 FEATURE:  
 NAME/KEY: cDNA encoding mutant urease  
 LOCATION: Modification at position 1312 to  
 IDENTIFICATION METHOD: Sequencing  
 OTHER INFORMATION:  
 687-645B-1

Patent Scores:  
 No.: 1.5e-52 Length: 2400  
 :  
 Similarity: 474.00 Matches: 103  
 Local Similarity: 64.76% Conservative: 33  
 Match: 49.05% Mismatches: 58  
 Indels: 16 Gaps: 4

904-994B-2 (1-226) x US-08-687-645B-1 (1-2400)

1 ValValLeuThrProLysGluGlyLysPheLeuLeuTyrTyrAlaGlyGluValAla 20  
 :  
 31 ATGGAACTGAGCCCGGAGAAAGACGCTTGCTTACCGCCGCGCTGGTGGCG 90

21 ArgLysArgLysAlaGluGlyIleLysIleAsnGlnProGluAlaAlaAlaTyrIleSer 40  
 ::  
 91 GAGCCTTATTAATGGAGGGCTCGGAGCTCACTATCGGAACCGCGGCCGTCAGC 150

41 AlaHistLeMetAspGluAlaArgArgGlyLysThrValAlaGlnLeuMetGluGlu 60  
 ||||| ||||| :  
 151 GCCTTTATTATGGAGGGCTCGGAGCTCACTATCGGAACCGCGGCCGTCAGC 207

61 CysMetHisPheLeuLysLysAspGluValMetProGlyValGlyAsnMetValProAsp 80

---

Db 208 GCGCTGCGCTGTGACCGCGAGCGATGAGGCGTCCGGAATAGTCGCGAT 267  
 Qy 81 LeuGlyValGluAlaThrPheProAspGlyThrLysLeuValThrValAsnTrpProle 100  
 Db 268 ATCCAGGTGAAAGCCACCTTCCGGACGCCGCTGCAAGCTGGTACACCGGTT 327  
 Qy 101 -----GlutProAspGlu-----HisPheLysAlaGlyGluLallyPhe 113  
 Db 328 ATCTGAGGTAGGCCATATCCCGGTTAATACGTTAACCGCGGAG----- 378  
 Qy 114 GlyCysAspLysAspIleGluIeuAsnAlaGlyLysGluValAlaGluValThr 133  
 Db 379 -----ArgCCCCTGAACTAACCGCCGCGGAACTGTGCGGTGGGTTG 423  
 Qy 134 AspGluGlyProLysSerLeuHisValGlySerHisPheHisPheGluLalaLys 153  
 Do 424 AACCGCCGATCGGCCATTCKGGTGGTGCACATTCGCCGAGGTAAACCG 483  
 Qy 154 AlanLysPheAspPheAspGluLysAlaTyrGluLysGluValAlaGluVal 173  
 Do 484 GCCTGAAGTCGACCGPCTAGGGCCGCTATGCCGTAATACCGGGGSCACG 543  
 Qy 174 ThrLeuArgIleGlyAlaGlyGlnThrArgLysValGlnLeuIleProLeuGlyLys 193  
 Do 544 GCGGTACCTTGAACCGGCCGAAAGCGGAGTCGACTGGTGGCTCCGGGTCAC 603  
 Qy 194 LysLysValIleGlyMataTyrGlyLeuVal 203 .  
 Do 604 CGCGCGCTTCGCTCGCGCGCGAGGTG 633

RESULT 13  
 US-07-732-242C-8  
 ; Sequence 8, Application US/07732242C  
 ; Patent No. 5299399  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Uozumi, Takeshi; Masaki Haruhiko;  
 ; APPLICANT: Hidaka, Makoto; Nakamura, Akira;  
 ; TITLE OF INVENTION: Gene of Urease  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Frieschauf, Holtz, Goodman & Woodward, P.C.  
 ; STREET: 600 Third Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10016-2088

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 0.72mb  
 COMPUTER: IBM PC compatible (NEC FC-9801 RX)  
 OPERATING SYSTEM: MS DOS  
 SOFTWARE: ASCII Form  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/732, 242C  
 FILING DATE: 19910718  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JPN 2-210178  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goodman, Herbert  
 REGISTRATION NUMBER: 17081  
 REFERENCE/DOCKET NUMBER: 910532/HG  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 972-1400  
 TELEX: (212) 370-1622  
 TELE: 236268

INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6131 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: both



Alignment Scores:  
 Pred. No.: 3.79e-47  
 Score: 467.00  
 Percent Similarity: 61.61%  
 Best Local Similarity: 42.86%  
 Query Match: 39.54%  
 DB: 4  
 Gap: 3

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Db 564511 ACAAGGACAAAGATATGATCCAGCGAATCAATA--GCCGAGGGATATCTC 564455  
 Qy 121 LeuAsnAlaGlyLysGluValThrGluLeuGluValThrAspGluGlyProlySerLeu 140  
 Db 564454 GCTAACTCGGGAAGAACCTTAATGCAAGTCAATTCTGCGACGCCAATT 564395  
 Qy 141 HisValGlySerHisPheHisPheGluLaAsnLysAlaLeuLysPheAspArgGlu 160  
 Db 564394 CAAGTGCTCCGATTCACATTGTTGAAACCAATATGCCCTAAATTGACCGACT 564335  
 Qy 161 LysAlaTygGlyLysArgLeuAspIleProSerGlyAsnThrLeuGlyLysGlyAlaGly 180  
 Db 564334 TTGGCACGTGGATGCCTTAATGTCATCTGGCATGCGGTGCGCTTGGTACCCGGT 564275  
 Qy 181 GluThrArgLysValGlnLeuIleProLeuGlyGlySerIleLysValLeuGlyMetAsn 200  
 Db 564274 GAGTGAAATCGTGGATTAGTGCTTGTGGTACCAAATCATTTAGTTCCAT 564215  
 Qy 201 GlyLeuValAsn 204  
 Db 564214 AATCAATTGAT 564203

RESULT 15  
 US-09-643-990A-1/C

; Sequence 1, Application US/09643990A  
 ; Parent No. 6228289  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert D. Fleischmann  
 ; Mark D. Adams  
 ; Owen White  
 ; Hamilton O. Smith

TITLE OF INVENTION: The Nucleotide sequence of the *Haemophilus influenzae* Rd Genome, Fragments  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville,  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3 1/2 inch diskette  
 COMPUTER: Dell Pentium  
 OPERATING SYSTEM: MS DOS v6.22  
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/643,990A  
 FILING DATE: 23-Aug-2000  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/487,429  
 FILING DATE: 1995-06-07  
 APPLICATION NUMBER: 08/426,787  
 FILING DATE: 1995-04-21

ATTORNEY/AGENT INFORMATION:  
 NAME: Kenley K. Hoover  
 REGISTRATION NUMBER: 40,302  
 REFERENCE/DOCKET NUMBER: PB186PC1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-610-5790  
 TELEFAX: 310-309-8439  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCER CHARACTERISTICS:  
 LENGTH: 183121 base Pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-643-990A-1

Search completed: February 16, 2005, 00:59:42  
 Job time : 905.667 sec

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Om nucleic - protein search, using frame\_plus\_n2p model

Run on: February 15, 2005, 20:03:24 ; Search time 31.5 Seconds  
 (without alignments) 13664.333 Million cell updates/sec

Title: US-09-904-994B-1

Perfect score: 5.47

Sequence: 1 rrgragatttcccaractt.....aaaaaaatggaaaggcacagg 2883

Scoring table: BL0SUM62

Xgapop	Ygapext	Ygapop	Fgapext	Delop
10.0	0.5	6.0	7.0	6.0 , Delext 7.0

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 648760

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Maximum Match 0%

Listing first 45 summaries

Command line parameters:

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-MODEL[frame_n2p model] -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US090404994/runat_11022005_134936_22927/app/query.fasta_1.3079
-DB=Issued_Patents_AA -QPM=fastan -SufFix=rai -MINMATCH=0.1 -LOOPPCL=0
-LOOPEXT=0 -UNITS=512 -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -INFILE=ext -HEAPSIZEMAX=500 -MINLEN=100
-USER=US090404994@CGN_1_1_26@runat_11022005_134936_22927 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database :

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backFiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	281.5	5.5	100	1 US-08-967-513-3 Sequence 3, Appli
2	281.5	5.5	100	2 US-08-687-645B-3 Sequence 3, Appli
3	269.5	5.2	99	1 US-07-732-242C-1 Sequence 1, Appli
4	261.5	5.1	100	2 US-08-467-822-23 Sequence 23, Appli
5	261.5	5.1	100	3 US-08-433-697-23 Sequence 23, Appli
6	261.5	5.1	100	3 US-08-466-248-23 Sequence 23, Appli
7	250.5	4.9	100	4 US-03-602-77A-18 Sequence 18, Appli
8	250.5	4.7	92	4 US-03-252-991A-17446 Sequence 17446_A
C	9	78.5	1.5	95 4 US-09-328-352-4313 Sequence 4313_AP
C	10	77	1.5	15 2 US-01-928-081-1 Sequence 1, Appli
C	11	77	1.5	15 4 US-09-338-922-1 Sequence 1, Appli
C	12	71.5	1.4	93 4 US-09-489-039A-7356 Sequence 7356_AP

ALIGNMENTS

RESULT 1

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; Sequence 3, Application US/08967513
; Patent No. 5783436
; GENERAL INFORMATION:
; APPLICANT: Robert P. Hausinger
; TITLE OF INVENTION: Mutant Urease and Method
; OF USE For Determination
; TITLE OF INVENTION: of Urea
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
```

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Worchester 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/967,513  
 FILING DATE: 11-NOV-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/687,645  
 FILING DATE: July 26, 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ian C. McLeod  
 REGISTRATION NUMBER: 20,931  
 REFERENCE/DOCKET NUMBER: MSU 4.1-309  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (517) 347-4100

TELEFAX: (517) 347-4103  
 TELEFAX: No. 5783436e  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 100  
 TYPE: amino acids  
 STRANDEDNESS: Single  
 MOLECULE TYPE: Linear  
 DESCRIPTION: Protein  
 HYPOTHETICAL: No  
 ANTI-SENSE: No  
 ORIGINAL SOURCE:  
 ORGANISM: N/A  
 STRAIN: N/A  
 INDIVIDUAL ISOLATE: N/A  
 CELL TYPE: N/A  
 FEATURE:  
 NAME/KEY: subunit Urea  
 LOCATION:  
 IDENTIFICATION METHOD: Sequencing  
 OTHER INFORMATION: encoded Subunit of  
 OTHER INFORMATION: mutant urease  
 US-08-967-513-3:

Alignment Scores:  
 Pred. No.: 8.43e-19 Length: 100  
 Score: 281.50 Matches: 59  
 Percent Similarity: 77.00% Conservative: 18  
 Best Local Similarity: 59.00% Mismatches: 22  
 Query Match: 5.47% Indels: 1  
 DB: Gaps: 1

US-09-904-994B-1 (1-2883) x US-08-967-513-3 (1-100)

QY 206 GTGAAACTCACCCAAAGAGCAGAACGTTCTGTATATTATCGGGCGGAAGTGGCT 265  
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 1 MetGluleuthrProArgGluLysAspLysLeuLeuPheThrAlaAlaLeuValAla 20

Db 41 AlaphelMetGluglyAlaArgAspGly--LyserValAlaSerLeuMetGluGlu 59

QY 266 AGAAAGCCAAAGCAGAGGGCTTAAGCTCAACACCCAGAACGCCATGGCTACATTAGT 325  
 :::::::::::::::::::::|||||:::|||||:::|||||:::|||||:::|||||:  
 21 GluArgArgLysAlaArgLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuSer 40

Db 326 GCCATATTATGGACGAGGGCGCTGGAAAAAACCGTGCCAGCTTATGGAGAG 385  
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 41 AlaphelMetGluglyAlaArgAspGly--LyserValAlaSerLeuMetGluGlu 59

QY 386 TCCATGCACTTTGAAAAAAGATGAGTAGTAAATGCCGGGGGGTATAATGGTCCGGAT 445  
 :::::::::::::::::::::|||||:::|||||:::|||||:::|||||:  
 60 GlyArgGlyValLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeu 79

Db 446 CTAGGCTAGAGGCCACCTCTCTGAGTGTAGAACCTGAACTCTGAACTGGCCCATC 505  
 :::::::::::::::::::::|||||:::|||||:::|||||:::|||||:  
 80 IleGlnValGluAlaThrProAspGlySerIleUvaIValThrValHisAsnProle 99

RESULT 2  
 US-08-687-645B-3

; Sequence 3, Application US/08687645B  
; Patent No. 5546752  
; GENERAL INFORMATION:  
; APPLICANT: Robert P. Hausinger;  
; TITLE OF INVENTION: Mutant Urease and Method  
; TITLE OF INVENTION: Of Use For Determination  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48864

COMPUTER READABLE FORM:

ATTORNEY/AGENT INFORMATION:  
 NAME: Ian C. McLeod  
 REGISTRATION NUMBER: 20,931  
 REFERENCE/DOCKET NUMBER: MSU 4.1-309  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (517) 347-4100  
 TELEFAX: (517) 347-4103  
 TELEX: No. 5846752  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 100  
 TYPE: amino acids  
 STRANDEDNESS: Single  
 MOLECULE TYPE: Linear  
 DESCRIPTION: Protein  
 HYPOTHETICAL: No  
 ANTI-SENSE: No  
 ORIGINAL SOURCE:  
 ORGANISM: N/A  
 STRAIN: N/A  
 INDIVIDUAL ISOLATE: N/A  
 CELL TYPE: N/A  
 FEATURE:  
 NAME/KEY: subunit Urea  
 LOCATION:  
 IDENTIFICATION METHOD: Sequencing  
 OTHER INFORMATION: encoded subunit of  
 OTHER INFORMATION: mutant urease  
 US-08-687-645B-3

Alignment Scores:  
 Pred. No.: 8.43e-19 Length: 100  
 Score: 281.50 Matches: 59  
 Percent Similarity: 77.00% Conservative: 18  
 Best Local Similarity: 59.00% Mismatches: 22  
 Query Match: 5.47% Indels: 1  
 DB: Gaps: 1

US-09-904-994B-1 (1-2883) x US-08-687-645B-3 (1-100)

QY 206 GTGAAACTCACCCAAAGAGCAGAACGTTCTGTATATTATCGGGCGGAAGTGGCT 265  
 :::::::::::::::::::::|||||:::|||||:::|||||:::|||||:::|||||:  
 1 MetGluleuthrProArgGluLysAspLysLeuLeuPheThrAlaAlaLeuValAla 20

Db 41 AlaphelMetGluglyAlaArgAspGly--LyserValAlaSerLeuMetGluGlu 59

QY 266 AGAAAGCCAAAGCAGAGGGCTTAAGCTCAACACCCAGAACGCCATGGCTACATTAGT 325  
 :::::::::::::::::::::|||||:::|||||:::|||||:::|||||:  
 21 GluArgArgLysAlaArgLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuSer 40

Db 326 GCCATATTATGGACGAGGGCGCTGGAAAAAACCGTGCCAGCTTATGGAGAG 385  
 :::::::::::::::::::::|||||:::|||||:::|||||:::|||||:  
 41 AlaphelMetGluglyAlaArgAspGly--LyserValAlaSerLeuMetGluGlu 59

QY 386 TCCATGCACTTTGAAAAAAGATGAGTAGTAAATGCCGGGGGGTATAATGGTCCGGAT 445  
 :::::::::::::::::::::|||||:::|||||:::|||||:  
 60 GlyArgGlyValLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeu 79

Db 446 CTAGGCTAGAGGCCACCTCTCTGAGTGTAGAACCTGAACTGGCCCATC 505  
 :::::::::::::::::::::|||||:::|||||:::|||||:  
 80 IleGlnValGluAlaThrProAspGlySerIleUvaIValThrValHisAsnProle 99



**RESULT 5**  
US-08-432-697-23  
Sequence 23, Application US/0843297  
Patent No. 6248330

**GENERAL INFORMATION:**

APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sébastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTON, POLYPEPTIDES FOR USE IN THE COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSE: Finnegan, Henderson, Farabow, Garrett & STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,697  
FILING DATE: 02-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:  
LENGTH: 100 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-432-697-23

**RESULT 6**  
US-08-466-248-23  
Sequence 23, Application US/08466248  
Patent No. 6258359

**GENERAL INFORMATION:**

APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sébastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTON, POLYPEPTIDES FOR USE IN THE COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSE: Finnegan, Henderson, Farabow, Garrett & STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,248  
FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:  
LENGTH: 100 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-466-248-23

**RESULT 7**  
US-08-466-248-23  
Sequence 23, Application US/08466248  
Patent No. 6258359

**GENERAL INFORMATION:**

APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sébastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTON, POLYPEPTIDES FOR USE IN THE COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSE: Finnegan, Henderson, Farabow, Garrett & STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,248  
FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:  
LENGTH: 100 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-466-248-23

**RESULT 8**  
US-09-904-994B-1 (1-2883) x US-08-432-697-23 (1-100)  
QY 206 GAGAACTCACCCAAAGAGAAGAAAGTTCTGTATATGGGGCGAAGTCGCT 265



PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17446  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: *Pseudomonas aeruginosa*  
; US-09-252-991A-17446

Alignment Scores:  
Pred. No.: 7.43 Length: 92  
Score: 87.50 Matches: 36  
Percent Similarity: 37.76% Conservative: 18  
Best Local Similarity: 25.17% Mismatches: 24  
Query Match: 1.70% Indels: 65  
DB: Gaps: 7

US-09-904-994B-1 (1-2883) x US-09-252-991A-17446 (1-92)

Qy 2101 AGCGCTACATCTCCAAATACACTATCACCCGCTTGACCCACGGCGTGAAGCAGATA 2160  
Db 6 SerAlaThrSerProSerLeuSerAlaProProAla-----AlaserSer 20

Qy 2161 TCGGCTCTGTCGAGAGGGCAAGATGCCGACTTGGGGTGGGAATCCGCTTGTG 2220  
Db 21 SerSerSerTyrLysArgSerAla----- 28

Qy 2221 GCGTAACACCCAAATCGTACAAGGGGTTATGGTGTCTCTGAATGGGGATT 2280  
Db 29 -----AlaAlaAlaArgTrpSerVal 35

Qy 2281 CTAAACGGCTCTGCCACTCCCCAACGGTTTATTACCGCCAAATGGCATCACG 2340  
Db 36 -----ThrArgCysMet----- 39

Qy 2341 GCGAGSGGAATTTGACACCACATCACTTGTGTTCCAAGTCGCCTATGAAATGGG 2400  
Db 40 -----SerAlaLysSerCysSerSerProAlaLysSerAla 51

Qy 2401 TCAAAG-----AAAAGCTGGCTAGAGCGCCAAAGTCTACCGGTCAAATGCC 2451  
Db 52 AlaLysArgArgSerArgSerTyrArg-----ArgSerCysThrSer 65

Qy 2452 GTAACATCACCAGAGAACCTCAAGTCACGACAAACGCCAAATCCGRCATC 2511  
Db 66 AlaserSerProGlyLysThrSerAlaAsnTrp-----ArgSerAlaProLysIle 83

Qy 2512 CGAACCT 2520  
Db 84 ArgValPro 86

RESULT 10  
US-08-928-081-1  
; Sequence 1, Application US/08928081  
; Parent No. 598531  
; GENERAL INFORMATION:  
; APPLICANT: Soman, Gopalan  
; APPLICANT: Thomas, Jr., William D.  
; APPLICANT: Monath, Thomas P.  
; TITLE OF INVENTION: Stabilization of  
; TITLE OF INVENTION: Helicobacter Urease  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Ebing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: PasteSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,081  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 06132/023001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-428-0200  
; TELEX: 617-428-7045  
; TELE:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-09-328-352-4313  
; Sequence 1, Application US/09328352  
; Parent No. 652958  
; General Information:  
; Applicant: Gary L. Breton et al.  
; Title of Invention: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; File Reference: GPC99-03PA  
; Current Application Number: US/09/328,352  
; Current Filing Date: 1999-06-04  
; Number of Seq ID Nos: 8252  
; Seq ID No 4313  
; Length: 96  
; Type: PRT  
; Organism: *Acinetobacter baumannii*  
; US-09-328-352-4313

Alignment Scores:  
Alignment: 57.8 Length: 96  
Pred. No.: 78.50 Matches: 22  
Score: 41.35% Conservative: 21  
Percent Similarity: 21.15% Mismatches: 32  
Query Match: 1.53% Indels: 29  
DB: Gaps: 3

Best Local Similarity: 21.15% Mismatches: 32  
Query Match: 1.53% Indels: 29  
DB: Gaps: 3

US-09-904-994B-1 (1-2883) x US-09-328-352-4313 (1-96)

Qy 1381 GGACCTGGCCCTCCAAACATGGTGTACGCCATTGGTAGGGCTPAGGAATT 1322  
Db 9 GlyAspValProProPro----- 15

Qy 1321 TGTGGAGAAAGGAAGTGGGTGTGAAATGCCGCGTATAATCATACTCC 1262  
Db 15 -----IleMetProProValThrProProIleSerValThrThr 28

Qy 1261 CCTGCTAGTCTCTGCGCCACCCACACCCATGAGGGCTAACGCCATCTGCGT 1202  
Db 29 ProArgGlyLeuSerProProThrProPro-----ValThrProProIle 44

Qy 1201 TCCTGTTCTGCCATGCCATGGATTGCCGTTAACCCAAATGUGGCT 1142  
Db 45 SerValIleThrSerSerGlyLeuProSerThrProProValThrProProIleThr 64

Qy 1141 TTGTAATCCGGTGTAGTCGATA-----ATCATGGCTTAGTGTGACT 1097  
Db 65 ValThrLeuProAlaThrProValThrProValAlaValValProProValleSer 84

Qy 1096 AAATCTAGGGG 1085  
Db 85 ValSerArgIle 88

Alignment Scores: 71.50  
Pred. No.: 27 Score: 77.00 Length: 15  
Percent Similarity: 93.33% Matches: 13  
Best Local Similarity: 86.67% Conservative: 1  
Query Match: 1.50% Mismatches: 1  
DB: 2 Indels: 0 Gaps: 0

US-09-904-994B-1 (1-2883) x US-09-489-039A-7356 (1-93)

Qy 1527 GAAGCGGCGCGGCGTGTAAATTGCGATGAGACTGGCGACCA 1571  
Db 1 GluAlaGlyAlaLeGlyPheAlaIleHisGluAspTrpGlyThr 15

RESULT 11

; Sequence 1, Application US/0938920B  
; Patent No. 6709851  
; GENERAL INFORMATION:  
; APPLICANT: Soman, Gopalan  
; APPLICANT: Thomas, William D., Jr.  
; APPLICANT: Monath, Thomas P.  
; TITLE OF INVENTION: Stabilization of Helicobacter Urease  
; FILE REFERENCE: 06132/022002  
; CURRENT APPLICATION NUMBER: US/09/338,920B  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: US 08/928,081  
; PRIOR FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Helicobacter pylori

US-09-338-920B-1

Alignment Scores: 77.00 Length: 15  
Pred. No.: 27 Score: 93.33% Matches: 13  
Percent Similarity: 93.33% Conservative: 1  
Best Local Similarity: 86.67% Mismatches: 1  
Query Match: 1.50% Indels: 0  
DB: 4 Gaps: 0

US-09-904-994B-1 (1-2883) x US-09-338-920B-1 (1-15)

Qy 1527 GAAGCGGCGCGGCGTGTAAATTGCGATGAGACTGGCGACCA 1571  
Db 1 GluAlaGlyAlaLeGlyPheAlaIleHisGluAspTrpGlyThr 15

RESULT 12

US-09-489-039A-7356

; Sequence 1, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 12832  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-12832

Alignment Scores: 374  
Pred. No.: 6610836 Score: 70.00 Length: 89  
Percent Similarity: 46.07% Matches: 27  
Best Local Similarity: 30.34% Conservative: 14  
Query Match: 1.36% Mismatches: 22  
DB: 4 Indels: 26  
Gaps: 5

US-09-904-994B-1 (1-2883) x US-09-489-039A-12832 (1-89)

Qy 645 TGAATAATGCTACCCACATGCAAGGATTAGGC---CCTTCATTAGTAACTCAAGTCAGTCG 589  
Db 2 TrpLysThrAlaLysProArgArgAlaGlyThrThrSerPheIleThrSerPro 21

SEQ ID NO 7356  
; LENGTH: 93  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-7356

Alignment Scores: 274  
Pred. No.: 274 Length: 93

US-09-904-994B-1 (1-2883) x US-09-489-039A-7356 (1-93)

Qy 1861 TGGTGGCATGTCATGAGATGCTAACGTTCTGCAACGTAATGCTATGGGATA 1802  
Db 55 -----CySalaCysSerAlaIleCysAlaIleThrProArgSerTyrValleSerIleAlaile 41  
Qy 1801 GTGGGGGGGGGGAGAGATATGAGCTCGCCATGGGATAACATCAGT 1742  
Db 68 SerIleSerSerSerIleGlyArgGlnIleSerAlaMtaAlaIleThr----- 84  
Qy 1741 GAGGTCTCTCACCGCTCCATGATGCG 1712  
Db 85 ArgCysSerMetPro---ProGluSerIleP 93

RESULT 13

US-09-489-039A-12832

; Sequence 1, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 12832  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-12832

Alignment Scores: 374  
Pred. No.: 6610836 Score: 70.00 Length: 89  
Percent Similarity: 46.07% Matches: 27  
Best Local Similarity: 30.34% Conservative: 14  
Query Match: 1.36% Mismatches: 22  
DB: 4 Indels: 26  
Gaps: 5

US-09-904-994B-1 (1-2883) x US-09-489-039A-12832 (1-89)

Qy 588 GTRACTCTTGCTGCAATGAGCTGATGCTTATGCCAACCAAATTCACTTCGCCC 529  
Db 2 TrpLysThrAlaLysProArgArgAlaGlyThrThrSerPheIleThrSerPro 21  
Qy 528 GCTTGAACTGCTCATCGTGTGATGGCCAAATTCAAGTTACAAGTTGCTACATCA 469  
Db 34 AlaLeMetArgSerSerValAspPheProGln-----ProGlu 46

GENERAL INFORMATION:  
 APPLICANT: Pompejus, Markus  
 APPLICANT: Kroger, Burkhard  
 APPLICANT: Schröder, Harwig  
 APPLICANT: Zeller, Oskar  
 APPLICANT: Haberhauer, Gregor

TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 INVOLVED IN HOMOSTASIS AND ADAPTATION

TITLE OF INVENTION: CORNYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 CURRENT APPLICATION NUMBER: DE 19931636.8

CURRENT FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/141,031

PRIOR FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: DE 19931636.8

PRIOR FILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: DE 19932125.6

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932126.4

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932127.2

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932128.0

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932129.9

PRIOR FILING DATE: 1999-07-19

PRIOR APPLICATION NUMBER: DE 19932226.0

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932920.6

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19932922.2

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19932924.9

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19932928.0

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19932930.3

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19932933.8

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19932935.4

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19932973.7

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19933002.6

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19933003.4

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19933005.0

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19933006.9

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19941378.9

PRIOR FILING DATE: 1999-08-31

PRIOR APPLICATION NUMBER: DE 19941379.7

PRIOR FILING DATE: 1999-08-31

PRIOR APPLICATION NUMBER: DE 19942088.2

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 442

SEQ ID NO 12

LENGTH: 40

Alignment Scores:  
 Pred. No.: 327  
 Score: 69.50  
 Percent Similarity: 48.89%  
 Best local Similarity: 31.11%

TYPE: PRT

ORGANISM: Corynebacterium glutamicum

US-09-602-777A-12

RESULT 15

US-09-602-777A-12

; Sequence 12, Application US/09602777A

; Patent No. 6831165

Qy 468 GCA-----AACGTGCTTCACCCCTAGA-----TCGGGA 439  
 Db 47 GlyProThrLysThrAlaAsnSerProSerSerLeuSerArgLeuThrTrpCysSerVal 66  
 Qy 438 ACATATTACCCACCCGGGTRACT 412  
 Db 67 ThrValLeuProAsnLeuLeuValThr 75

RESULT 14

US-09-328-352-4788

; Sequence 4788, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:  
 APPLICANT: Gary L. Breton et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE REFERENCE: GTCC99-03PA

CURRENT APPLICATION NUMBER: US/09/328, 352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4788

LENGTH: 99

TYPE: PRT

ORGANISM: Acinetobacter baumannii

US-09-328-352-4788

Alignment Scores:  
 Pred. No.: 49.9 Length: 99  
 Score: 69.00 Matches: 33  
 Percent Similarity: 32.65% Conservative: 15  
 Best local Similarity: 22.45% Mismatches: 37  
 Query Match: 1.34% Indels: 62  
 DB: 4 Gaps: 8

US-09-904-994B-1 (1-2883) x US-09-328-352-4788 (1-99)

Qy 1573 GTGTGCCCCACTCTCATGCATTAAACCAATCGGCCGCTTACTGTCTACA 1514  
 Db 1 IleLeuProValSer----GlyLeuSerProArgSerPro----- 12

Qy 1513 AGTTGTTTTCTAGCTATGGCTTGCCTTGCCAAAAGCCACATTCATAGATACTCT 1454  
 Db 13 -----PrometProPrometProProMetPro----- 22

Qy 1453 TCTGCTGGCGAACATGGGCAAGTTCCTTGCCTTGCCGAGCTAGTAGTCGCGATT 1394  
 Db 23 -----ValleGlyLeuValle 28

Qy 1393 GTGCCATCTACGGACCTGTGCCCT-----CCA 1364  
 Db 29 SerProSerPro---ProleProProMetIleProvalleGlyLeuValleSerPro 47

Qy 1363 AACATGGGTGTAACGCCATTGGCTAGAGCGGGATTGTGTGAGAAGGAAGTGG 1304  
 Db 48 SerProProleProProleThrProValleGly----- 59

Qy 1303 GTGTGTCATCCATTCCCCACGGTATAACATACCTCCCTGCTAGTGCTGTG 1244  
 Db 60 -----ProlylSerProValleGlyLeuValleGly----- 73

Qy 1243 CCCACACCACGACCATATGAGGGCT-----ACCCCATCTTGCTGTCTG 1196  
 Db 74 GluLeuProAsnThrLeuLeuIleValleGlyLeuValleGlyLeuValleGlyLeu 93

Qy 1195 TTTCCTGCTCCATGCA 1175  
 Db 94 LeuPro--LeuProMetPro 99

US-09-602-777A-12

Alignment Scores:  
 Pred. No.: 327 Length: 40  
 Score: 69.50 Matches: 14  
 Percent Similarity: 48.89% Conservative: 8  
 Best local Similarity: 31.11% Mismatches: 16

Query Match:	1. 33%	Indels:	7
DB:	4	Gaps:	1
US-09-904-994B-1 (1-2883) x US-09-602-777A-12 (1-40)			
QY 509 CGAGATGCACTTCAAACGGCGAACGTGAATTGGTTGGCTTAAGACATGGAGC C 568			
Db 3 ProlyglutylutileLeusSerGluSerLeutThrGly----- 15			
QY 569 ATGGAGGAAAGAGTAACCGAACCTGGTTACTAATGAGGCCCTAAACCTTGCA T 628			
Db 16 AsnValGlyArgGluAlaLysThrIleGluIleAsnThrGlyAspArgProValGln 35			
QY 629 GTGGGTAGGCCATTTC 643			
Db 36 IleGlySerHisPhe 40			

Search completed: February 15, 2005, 20:34:27  
Job time : 36.5 secs

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